

138738
SEARCH REQUEST FORM

Access DB# _____

Scientific and Technical Information Center

CRFF

Requester's Full Name: DAVID A. SAUNDERS Examiner #: 64910 Date: 11/26/04
Art Unit: 1644 Phone Number: 301-272-0849 Serial Number: 10/089,700
Mail Box and Bldg/Room Location: REM 3C70 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: DIAGNOSTIC AND THERAPEUTIC EPITOPE AND TRANSGENIC PLANT

Inventors (please provide full names): ROBERT P ANDERSON, ANDRIAN HILL,
DEREK P JEWELL

Earliest Priority Filing Date: 10/01/99 (GB) 10/02/2000 (PCT, PUBLISHED AS WO 01/25793)

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

PLEASE SEARCH SEQ ID NOS 1 & 2 (1 IS A SUB-SEGMENT OF 2). THESE ARE BOTH SUB-SEQUENCES OF GLIADIN (SEQ ID NO: 3) WITH A MUTATION AT POSITION 65 FROM GLN TO GLU. I AM ONLY INTERESTED IN HITS THAT HAVE THIS MUTATION. THUS, YOU MAY WANT TO DO AN EXACT SEARCH FOR SEQ ID NOS: 1 AND/OR 2.

PLEASE SEARCH SEQ ID NO: 3 (GLIADIN), IF POSSIBLE PLEASE SEARCH THIS WITH EACH OF THE FOLLOWING SUBSTITUTIONS AT POSITION 65 IN PLACE OF GLN:
HIS, ⁸⁰TYR, ⁸¹TRP, ⁸²LYS, ⁸³PRO, ⁸⁴ARG. OTHERWISE YOU WILL LIKELY GET A LARGE NO. OF HITS FOR THE UNALTERED GLIADIN.

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OW protein - protein search, using sw model

Run on: December 15, 2004, 15:22:18 ; Search time 152 Seconds

(without alignments)
16.520 Million cell updates/sec

Title: US-10-089-700-1

Perfect score: 42

Sequence: 1 P0P0LFPY 7

Scoring table: BLOSUM62

Searched: 2002273 seqs, 358729239 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 100%

Maximum Match: 100%

Listing first 500 summaries

Database :
1: Genesep235004:*
2: Genesep235004:*
3: Genesep235004:*
4: Genesep235004:*
5: Genesep235004:*
6: Genesep235004:*
7: Genesep235004:*
8: Genesep235004:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	7	AAU01797	AAU01797 Wheat A-g
2	42	100.0	7	ADP91448	ADP91448 Immunogen
3	42	100.0	7	ADP91337	ADP91337 High affi
4	42	100.0	7	ADH14511	ADH14511 Gliadin r
5	42	100.0	9	ADP91460	ADP91460 T-cell ep
6	42	100.0	9	ADP91462	ADP91462 T-cell ep
7	42	100.0	9	ADP91464	ADP91464 Immunogen
8	42	100.0	9	ADP91461	ADP91461 T-cell ep
9	42	100.0	9	ADP19619	ADP19619 Antigenic
10	42	100.0	9	ADP19623	ADP19623 Antigenic
11	42	100.0	9	ADP19620	ADP19620 Antigenic
12	42	100.0	10	ADP91449	ADP91449 Immunogen
13	42	100.0	11	AAU01811	AAU01811 Wheat A-g
14	42	100.0	11	ADH14524	ADH14524 Gliadin r
15	42	100.0	11	ADH14524	ADH14524 Gliadin r
16	42	100.0	12	AAU01827	AAU01827 Alpha-Gli
17	42	100.0	12	AAU01809	AAU01809 Wheat aip
18	42	100.0	12	AAE38560	AAE38560 Wheat pep
19	42	100.0	12	ADP91475	ADP91475 Peptide f
20	42	100.0	12	ADH14576	ADH14576 Gliadin r
21	42	100.0	12	ADH14559	ADH14559 Gliadin r
22	42	100.0	12	ADH14573	ADH14573 Gliadin r
23	42	100.0	12	ADH16186	ADH16186 Gliadin r
24	42	100.0	12	ADH14523	ADH14523 Gliadin r
25	42	100.0	12	ADH14571	ADH14571 Gliadin r

ALIGNMENTS

26	42	100.0	12	ADH14648	ADH14648 Gliadin r
27	42	100.0	13	AAE38563	AAE38563 Wheat pep
28	42	100.0	13	ADP91447	ADP91447 Immunogen
29	42	100.0	13	ADP91450	ADP91450 Immunogen
30	42	100.0	13	ADP91349	ADP91349 High affi
31	42	100.0	13	ADH14656	ADH14656 Gliadin r
32	42	100.0	14	AAU01828	AAU01828 Alpha-Gli
33	42	100.0	14	AAE38564	AAE38564 Wheat pep
34	42	100.0	14	AAE38561	AAE38561 Wheat pep
35	42	100.0	14	ADH14649	ADH14649 Gliadin r
36	42	100.0	14	ADH14560	ADH14560 Gliadin r
37	42	100.0	14	ADH14577	ADH14577 Gliadin r
38	42	100.0	14	ADH14574	ADH14574 Gliadin r
39	42	100.0	14	ADH16188	ADH16188 Gliadin r
40	42	100.0	15	ADH14659	ADH14659 Gliadin r
41	42	100.0	15	ADH14658	ADH14658 Gliadin r
42	42	100.0	17	AAU01804	AAU01804 Wheat A-g
43	42	100.0	17	AAU01832	AAU01832 Gliadin r
44	42	100.0	17	AAU01843	AAU01843 Wheat pep
45	42	100.0	17	AAU01798	AAU01798 Wheat A-g
46	42	100.0	17	AAU01803	AAU01803 Wheat A-g
47	42	100.0	17	AAU01802	AAU01802 Wheat A-g
48	42	100.0	17	ADH14516	ADH14516 Gliadin r
49	42	100.0	17	ADH14564	ADH14564 Gliadin r
50	42	100.0	17	ADH14512	ADH14512 Gliadin r
51	42	100.0	17	ADH14635	ADH14635 Gliadin r
52	42	100.0	17	ADH16210	ADH16210 Gliadin r
53	42	100.0	17	ADH14518	ADH14518 Gliadin r
54	42	100.0	17	ADH16182	ADH16182 Gliadin r
55	42	100.0	17	ADH14557	ADH14557 Gliadin r
56	42	100.0	17	ADH14653	ADH14653 Gliadin r
57	42	100.0	17	ADH16183	ADH16183 Gliadin r
58	42	100.0	17	ADH14517	ADH14517 Gliadin r
59	42	100.0	17	ADH14633	ADH14633 Gliadin r
60	42	100.0	17	ADH14633	ADH14633 Gliadin r
61	42	100.0	17	ADH14539	ADH14539 Control p
62	42	100.0	17	ADH14538	ADH14538 Gliadin r
63	42	100.0	17	ADH14537	ADH14537 Control p
64	42	100.0	17	ADH14575	ADH14575 Gliadin r
65	42	100.0	20	AAU01807	AAU01807 Wheat A-g
66	42	100.0	20	ADH14521	ADH14521 Gliadin r
67	42	100.0	33	ADP91350	ADP91350 High affi

RESULT 1
AAU01797 standard; peptide; 7 AA.
AAU01797;
07-SEP-2001 (first entry)
Wheat A-gliadin derived oligopeptide T-cell epitope.
Wheat: A-gliadin; oligopeptide T-cell epitope; coeliac disease;
gluten intolerance; T-cell binding; antagonist; transglutaminase;
transgenic plant.
Triticum aestivum.
MO200125793-A2.
12-Apr-2001.
02-OCT-2000; 2000MC-GE003760.
01-OCT-1999; 99GB-00023306.
(ISIS-) ISIS INNOVATION LTD.

NO corresponding
to wheat
protein database

Anderson RP, Hill AVS, Jewell DP;
WPI; 2001-300179/31.
Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.

Claim 1; Page 6; 107pp; English.

The sequence is a wheat A-gliadin oligopeptide-T-cell epitope. The peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can be modified by transglutaminase to a sequence that comprises the epitope is useful for decreasing the ability of gliadin protein to cause coeliac disease. Nucleic acids encoding proteins antagonistic to the T-cell binding of the epitopes are useful for obtaining a transgenic plant cell or seed and for the production of a protein. The resultant crop plant is useful for obtaining a product of a wheat plant, especially grain, which is optionally processed into flour or another grain product. Food comprising the antagonistic protein is useful instead of a wild-type gliadin

Sequence 7 AA;

Query Match 100.0%; Score 42; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 POPELPY 7
1 POPELPY 7

RESULT 2
ADP91448
ADP91448 standard; peptide; 7 AA.

ADP91448;

26-FEB-2004 (first entry)

Immunogenic gluten oligopeptide.

Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic; gluten; Celiac Sprue; dermatitis herpeticiformis; HLA-DQ2 positive; type I diabetes; protein co-ordinate data.

Synthetic.

WO2003096984-A2.

27-NOV-2003.

14-MAY-2003; 2003WO-US015506.

14-MAY-2002; 2002US-0380761P.
28-JUN-2002; 2002US-0392782P.
31-OCT-2002; 2002US-0429333P.
20-NOV-2002; 2002US-0428033P.

(STRD) UNIV LELAND STANFORD JUNIOR.
(SOLL) SOLLID L M.

PA (HAUS/) HAUSCH F.
PA (SHAN/) SHAN L.
PA (KHOS/) KHOSLA C.
PA (QUAR/) QUARSTEN H.
PI Solid LM, Hausch F, Shan L, Khosla C, Quarsten H, Gray G;
PI Kim C;
XX
XX
DR WPI; 2004-053078/05.

PT New HLA-binding peptide inhibitor that is an analog of an immunogenic
PT gluten oligopeptide, useful for preparing a composition for treating
PT e.g., Celiac Sprue or dermatitis herpeticiformis.

Claim 5; Page 112; 115pp; English.

The invention relates to a new HLA-binding peptide inhibitor, which is an analog of an immunogenic gluten oligopeptide of at least about 8 residues in length, altered by the replacement of one or more amino acids and that binds tightly to HLA molecules, and is proteolytically stable and does not activate disease-specific T cells. Also disclosed is a computer for producing a three-dimensional representation of an HLA-DQ2 molecule bound to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor comprises the sequence PXPPELPY. The HLA-binding peptide inhibitor is useful for preparing a composition for treating Celiac Sprue or dermatitis herpeticiformis, or HLA-DQ2 positive individuals who are either predisposed to or have developed symptoms of type I diabetes. The current sequence represents an immunogenic gluten oligopeptide that may be modified to generate an HLA-binding peptide inhibitor.

Sequence 7 AA;

Query Match 100.0%; Score 42; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 POPELPY 7
1 POPELPY 7

RESULT 3
ADP91337
ADP91337 standard; peptide; 7 AA.

ADP91337;

26-FEB-2004 (first entry)

High affinity peptide substrate for tTGase.

Dermatological; neuroprotective; cytostatic; vulnery; anticonvulsant;
KW neurotropic; antiparkinsonian; tranquiliser; antiinflammatory;
KW immunosuppressive; celiac sprue; dermatitis herpeticiformis;
KW tissue transglutaminase; tTGase; inhibitor; gluten;
KW neurological disorder; cancer; wound healing; Huntington's disease;
KW Alzheimer's disease; Parkinson's disease; food intolerance.

Unidentified.

WO2003096979-A2.

27-NOV-2003.

14-MAY-2003; 2003WO-US015343.

14-MAY-2002; 2002US-0380761P.
28-JUN-2002; 2002US-0392782P.
31-OCT-2002; 2002US-0429333P.
20-NOV-2002; 2002US-0428033P.

(STRD) UNIV LELAND STANFORD JUNIOR.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:55:59 ; Search time 161.5 seconds
(without alignments)

37.761 Million cell updates/sec

Title: US-10-089-700-2

Perfect score: 97

Sequence: 1 QLOPFPQPELPPQPOS 17

Scoring table: BLOSUM62

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: Geneseqp23sep04:*
2: geneseqp1980s:*
3: geneseqp1990s:*
4: geneseqp2000s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	97	100.0	17	AAU01798	Aau01798 Wheat A-g
2	97	100.0	17	ADH14512	Adh14512 Gliadin r
3	97	100.0	17	ADH14635	Adh14635 Gliadin r
4	97	100.0	17	ADH16210	Adh16210 Gliadin r
5	97	100.0	17	ADH16182	Adh16182 Gliadin r
6	97	100.0	17	ADH14517	Adh14517 Gliadin r
7	97	100.0	17	ADH14633	Adh14633 Gliadin r
8	97	100.0	17	ADH14558	Adh14558 Gliadin r
9	97	100.0	17	ADH14575	Adh14575 Gliadin r
10	97	100.0	17	ADH14575	Adh14575 Gliadin r
11	97	100.0	20	AAU01807	Aau01807 Wheat A-g
12	97	100.0	20	ADH14521	Adh14521 Gliadin r
13	94	96.9	17	AAU01803	Aau01803 Wheat A-g
14	94	96.9	17	AAU01802	Aau01802 Wheat A-g
15	94	96.9	17	AAU01806	Aau01806 Wheat A-g
16	94	96.9	17	ADH14516	Adh14516 Gliadin r
17	94	96.9	17	ADH16184	Adh16184 Gliadin r
18	94	96.9	17	ADH16194	Adh16194 Gliadin r
19	94	96.9	17	ADH14520	Adh14520 Gliadin r
20	94	96.9	17	ADH14634	Adh14634 Gliadin r
21	94	96.9	17	ADH14697	Adh14697 Gliadin r
22	94	96.9	17	ADH14666	Adh14666 Gliadin r
23	94	96.9	17	ADH14517	Adh14517 Gliadin r
24	94	96.9	17	ADH14591	Adh14591 Gliadin r
25	94	96.9	17	ADH14660	Adh14660 Gliadin r

26	94	96.9	20	AAU01801	Aau01801 Wheat A-g
27	94	96.9	20	ADH14515	Adh14515 Gliadin r
28	94	96.9	266	AAU01799	Aau01799 Wheat A-g
29	94	96.9	266	ADH14513	Adh14513 A-gliadin
30	93	95.9	17	ADH14564	Adh14564 Gliadin r
31	93	95.9	17	ADH14537	Adh14537 Control P
32	93	95.9	33	ADP9150	Adp9150 High alt
33	93	93.8	17	AAU01804	Aau01804 Wheat A-g
34	91	93.8	17	ADH14518	Adh14518 Gliadin r
35	90	92.8	17	AAU01816	Aau01816 Wheat G11
36	90	92.8	17	AAU01817	Aau01817 Wheat G11
37	90	92.8	17	ADH16196	Adh16196 Gliadin r
38	90	92.8	17	ADH14671	Adh14671 Gliadin r
39	90	92.8	17	ADH14669	Adh14669 Gliadin r
40	90	92.8	17	ADH14536	Adh14536 Control P
41	90	92.8	17	ADH14593	Adh14593 Gliadin r
42	90	92.8	17	ADH14638	Adh14638 Gliadin r
43	90	92.8	17	ADH14592	Adh14592 Gliadin r
44	90	92.8	17	ADH16195	Adh16195 Gliadin r
45	90	92.8	17	ADH14782	Adh14782 Gliadin r

ALIGNMENTS

RESULT 1	AAU01798	AAU01798 standard; peptide; 17 AA.
ID	AAU01798	
XX	AAU01798:	
AC	07-SEP-2001 (first entry)	
DT		
XX		
DE	Wheat A-gliadin immunodominant T-cell epitope, A-gliadin 57-73 Q865.	
KW	Wheat; A-gliadin; immunodominant T-cell epitope; coeliac disease;	
KM	gluten intolerance; T-cell binding; antagonist; transglutaminase;	
KW	transgenic plant; A-gliadin 57-73 Q865.	
XX		
OS	Triticum aestivum.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 1	/label= Lys, Ala
FT		/note= "Optional"
FT	Misc-difference 2	/label= Lys, Ala
FT		/note= "Optional"
FT	Misc-difference 3	/label= Tyr, Trp, Ile, Gly, Ala, Ser, Lys, Pro, Glu
FT		/note= "Optional"
FT	Misc-difference 4	/label= Trp, Tyr, Ile, Ser, Ala, Gly, Glu, Lys
FT		/note= "Optional"
FT	Misc-difference 5	/label= Tyr, Ile, Trp, His, Leu, Ser, Thr, Met, Pro, Glu, Asn, Val, Asp, Ala, Arg, Lys, Glu
FT		/note= "Optional"
FT	Misc-difference 6	/label= Val, Tyr, Trp, Ile, Phe, Thr, Ser, Met, Leu, Glu, Ala, His, Arg, Lys, Gly, Asp, Asn, Glu
FT		/note= "Optional"
FT	Misc-difference 7	/label= Ser, Ile, Met, Leu, Val, His, Phe, Thr, Ala, Tyr, Glu, Asp, Asn, Gly, Trp, Lys, Arg, Pro
FT		/note= "Optional"
FT	Misc-difference 8	/label= Thr, Val, Ala, Ser, Tyr, Arg, Leu, Gly, Asp, Met, Ile, His, Trp, Phe, Asn, Glu, Lys
FT		/note= "Optional"
FT	Misc-difference 9	/label= Asp, Asn, Ala, Ser, Cys, His, Glu-Lys, Val, Gly, Ile, Thr, Glu, Leu, Phe, Met, Trp, Arg, Pro, Lys, Tyr

FT Misc-difference /note="Optional"
 10 /label= Met, Pro, Ile, Val, Gln, Phe, Tyr, Thr, Asn, His,
 Ser, Trp, Ala, Asp, Gly, Glu, Lys, Arg
 FT /note="Optional"
 FT Misc-difference 11 /label= Ser, Thr, Asn, Leu, Glu, Val, Ala, Asp, Met, Ile,
 His, Phe, Gly, Trp, Gln, Arg, Tyr, Lys
 FT /note="Optional"
 FT Misc-difference 12 /label= Val, Trp, Ile, Phe, Ala, Ser, Thr, Leu, Gln, His,
 Met, Asp, Gly, Asn, Glu, Arg, Pro, Lys
 FT /note="Optional"
 FT Misc-difference 13 /label= Ser, Thr, Ile, Asn, Tyr, Gly, Val, Ala, Phe, His,
 Met, Arg, Trp, Gln, Lys, Leu, Glu, Asp
 FT /note="Optional"
 FT Misc-difference 14 /label= Tyr, Trp, Ser, Ala, Gly, Glu, Ile, Lys, Pro
 15 /note="Optional"
 FT Misc-difference 15 /label= Lys, Ala
 16 /note="Optional"
 FT Misc-difference 16 /label= Lys, Ala
 17 /note="Optional"
 FT Misc-difference 17 /label= Lys, Ala
 /note="Optional"
 FT WO200125793-A2.
 12-APR-2001.
 02-OCT-2000; 2000WO-GB003760.
 01-OCT-1999; 99GB-00023306.
 (ISIS-) ISIS INNOVATION LTD.
 Anderson RP, Hall AVS, Jewell DP;
 WPI; 2001-300179/31.
 DR WPI; 2001-300179/31.
 XX Diagnosing coeliac disease or susceptibility to the disease in an
 XX individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.
 PS Claim 1; Page 6; 107pp; English.
 XX The sequence represents wheat A-gliadin immunodominant T-cell epitope, A-
 CC gliadin 57-73 Q865, where the Gln at a position corresponding to 65 in
 CC the full length A-gliadin has been converted to a Glu by the action of a
 CC transglutaminase. The peptides of the invention are used to test
 CC mammalian (preferably human) susceptibility to coeliac disease (gluten
 CC intolerance). The peptides are contacted with a blood sample and T cell
 CC recognition measured, a positive T-cell recognition indicating a
 CC susceptibility to coeliac disease. The peptides are useful for inducing
 CC tolerance in an individual, and antagonists to the peptides are useful for
 CC treating or preventing coeliac disease in an individual and for producing
 CC an antibody specific to them or a wild-type sequence. A mutant gliadin
 CC protein (or its fragment of 15 amino acids in length) whose wild-type
 CC sequence can be modified by transglutaminase to a sequence that comprises
 CC the epitope, but which has been modified in such a way that it does not
 CC contain sequence which can be modified by transglutaminase to a sequence
 CC that comprises the epitope is useful for transglutaminase to a sequence
 CC protein to cause coeliac disease. Nucleic acids encoding proteins
 CC antagonistic to the T-cell binding of the epitopes are useful for
 CC obtaining a transgenic plant cell or seed and for the production of a
 CC protein. The resultant crop plant is useful for obtaining a product of a
 CC wheat plant, especially grain, which is optionally processed into flour
 CC or another grain product. Food comprising the antagonistic protein is

CC useful instead of a wild-type gliadin
 XX
 XX Sequence 17 AA;
 SQ
 Query Match 100.0%; Score 97; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLCPPQPELPYPQPOS 17
 DB 1 QLCPPQPELPYPQPOS 17
 RESULT 2
 ADH14512
 ID ADH14512 standard; peptide; 17 AA.
 XX
 AC ADH14512;
 DT 11-MAR-2004 (first entry)
 XX
 DE Gliadin related epitope peptide SEQ ID NO:2.
 XX
 KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KW vaccine.
 XX
 OS Synthetic.
 XX
 PN WO2003104273-A2.
 PD 18-DEC-2003.
 XX
 PF 05-JUN-2003; 2003WO-GB002450.
 XX
 PR 05-JUN-2002; 2002GB-00012885.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX
 PI Anderson RP, Hall AVS, Jewell DP;
 DR WPI; 2004-043640/04.
 XX
 XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 PS Claim 1; SEQ ID NO 2; 177pp; English.
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 CC
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 97; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QLCPPQPELPYPQPOS 17
 DB 1 QLCPPQPELPYPQPOS 17

RESULT 3

ADH14635 standard; peptide; 17 AA.

ADH14635;

11-MAR-2004 (first entry)

Gliadin related epitope peptide.

coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

vaccine.

Synthetic.

WO2003104273-A2.

18-DEC-2003.

05-JUN-2003; 2003WO-GB002450.

05-JUN-2002; 2002GB-00012885.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2004-043640/04.

Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

cell receptor.

Example 2; Page 79; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor. To an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

Sequence 17 AA:

Query Match 100.0%; Score 97; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QLOPFPQPELPYPQPS 17

1 QLOPFPQPELPYPQPS 17

ADH16210 standard; peptide; 17 AA.

ADH16210;

11-MAR-2004 (first entry)

Gliadin related epitope peptide.

coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

vaccine.

Synthetic.

WO2003104273-A2.

18-DEC-2003.

05-JUN-2003; 2003WO-GB002450.

05-JUN-2002; 2002GB-00012885.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

Synthetic.

WO2003104273-A2.

18-DEC-2003.

05-JUN-2003; 2003WO-GB002450.

05-JUN-2002; 2002GB-00012885.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2004-043640/04.

Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

cell receptor.

Example 10; Fig 17; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor. To an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

Sequence 17 AA:

Query Match 100.0%; Score 97; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 QLOPFPQPELPYPQPS 17

1 QLOPFPQPELPYPQPS 17

ADH16182 standard; peptide; 17 AA.

ADH16182;

11-MAR-2004 (first entry)

Gliadin related epitope peptide.

coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

vaccine.

Synthetic.

WO2003104273-A2.

18-DEC-2003.

05-JUN-2003; 2003WO-GB002450.

05-JUN-2002; 2002GB-00012885.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

XX WPI, 2004-043640/04.
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX
PS Example 6; Fig 12a; 177pp; English.
CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 17 AA;
SC
Query Match 100.0%; Score 97; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLOPFPQPELPYPQPOS 17
DB 1 QLOPFPQPELPYPQPOS 17
RESULT 6
ADH14557
ID ADH14557 standard; peptide; 17 AA.
XX
XX ADH14557;
AC
XX 11-MAR-2004 (first entry)
DT
XX
XX Gliadin related epitope peptide.
DB
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KW vaccine.
XX
XX Synthetic.
OS
XX WO2003104273-A2.
EN
XX 18-DEC-2003.
ED
XX
XX 05-JUN-2003; 2003WO-GB002450.
FP
XX
XX 05-JUN-2002; 2002GB-00012885.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PI
XX Anderson RP, Hill AVS, Jewell DP;
PI
XX WPI, 2004-043640/04.
DR
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX Example 14; Page 65; 177pp; English.
PS
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 17 AA;
SC
Query Match 100.0%; Score 97; DB 8; Length 17;

CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 17 AA;
SC
Query Match 100.0%; Score 97; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1,1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLOPFPQPELPYPQPOS 17
DB 1 QLOPFPQPELPYPQPOS 17
RESULT 7
ADH14653
ID ADH14653 standard; peptide; 17 AA.
XX
XX ADH14653;
AC
XX 11-MAR-2004 (first entry)
DT
XX
XX Gliadin related epitope peptide.
DB
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KW vaccine.
XX
XX Synthetic.
OS
XX WO2003104273-A2.
EN
XX 18-DEC-2003.
ED
XX
XX 05-JUN-2003; 2003WO-GB002450.
FP
XX
XX 05-JUN-2002; 2002GB-00012885.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PI
XX Anderson RP, Hill AVS, Jewell DP;
PI
XX WPI, 2004-043640/04.
DR
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX Example 6; Page 80; 177pp; English.
PS
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 17 AA;
SC
Query Match 100.0%; Score 97; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPQPOS 17
DB 1 QLOPFPQPELPYPQPOS 17

RESULT 8

ADH14633
ID ADH14633 standard; peptide; 17 AA.

AC ADH14633;

DT 11-MAR-2004 (first entry)

DE Glutadin related epitope peptide.

KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

XX Example 15; Page 75; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 97; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPQPOS 17
DB 1 QLOPFPQPELPYPQPOS 17

RESULT 9

ADH14558
ID ADH14558 standard; peptide; 17 AA.

AC ADH14558;

XX 11-MAR-2004 (first entry)

DT Gliadin related epitope peptide.

DE coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

XX Example 14; Page 66; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 97; DB 8; Length 17;

Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPQPOS 17
DB 1 QLOPFPQPELPYPQPOS 17

RESULT 10

ADH14575
ID ADH14575 standard; peptide; 17 AA.

AC ADH14575;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

XX 05-JUN-2003; 2003WO-GB002450.
XX 05-JUN-2002; 2002GB-00012885.
XX (ISIS-) ISIS INNOVATION LTD.
XX Anderson RP, Hill AVS, Jewell DP;
XX WPI; 2004-043640/04.
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PR cell receptor.
XX
XX Example 14; Page 71; 177pp; English.
XX
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 17 AA;
SQ
Query Match 100.0%; Score 97; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLOPFPQPELPYPOQS 17
DB 1 QLOPFPQPELPYPOQS 17
RESULT 11
AAU01807
ID AAU01807 standard; peptide; 20 AA.
XX AAU01807;
XX
XX 07-SEP-2001 (first entry)
XX
XX Wheat A-gliadin 56-75 transglutaminase treated peptide.
XX
XX Wheat; A-gliadin; 56-75 peptide; coeliac disease; gluten intolerance;
XX T-cell binding; antagonist; transglutaminase; transgenic plant.
XX
XX Triticum aestivum.
XX
XX WO200125793-A2.
XX
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-GB003760.
XX
XX 01-OCT-1999; 99GB-00023306.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Anderson RP, Hill AVS, Jewell DP;
XX
XX WPI; 2001-300179/31.
XX
XX Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind

PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.
XX
XX Example 3; Page 40; 107pp; English.
XX
XX The sequence represents wheat A-gliadin 56-75 peptide, which has been
CC treated with transglutaminase resulting in the Gln at position
CC corresponding to 65 in the full length A-gliadin being converted Glu. The
CC peptides of the invention are used to test mammalian (preferably human)
CC susceptibility to coeliac disease (gluten intolerance). The peptides are
CC contacted with a blood sample and T cell recognition measured, a positive
CC T-cell recognition indicating a susceptibility to coeliac disease. The
CC peptides are useful for inducing tolerance in an individual and
CC antagonists are useful for inducing tolerance in an individual and
CC antagonists are useful for inducing tolerance in an individual and
CC disease in an individual and for producing an antibody specific to them
CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
CC amino acids in length) whose wild-type sequence can be modified by
CC transglutaminase to a sequence that comprises the epitope, but which has
CC been modified in such a way that it does not contain sequence which can
CC be modified by transglutaminase to a sequence that comprise the epitope
CC is useful for decreasing the ability of gliadin protein to cause Coeliac
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
CC binding of the epitopes are useful for obtaining a transgenic plant cell
CC or seed and for the production of a protein. The resultant crop plant is
CC useful for obtaining a product of a wheat plant, especially grain, which
CC is optionally processed into flour or another grain product. Food
CC comprising the antagonistic protein is useful instead of a wild-type
CC gliadin
XX
XX Sequence 20 AA;
SQ
Query Match 100.0%; Score 97; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QLOPFPQPELPYPOQS 17
DB 2 QLOPFPQPELPYPOQS 18
RESULT 12
ADH14521
ID ADH14521 standard; peptide; 20 AA.
XX ADH14521;
XX
XX 11-MAR-2004 (first entry)
XX
XX Gliadin related epitope peptide SEQ ID NO:11.
XX
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
XX vaccine.
XX
XX Synthetic.
XX
XX WO2003104273-A2.
XX
XX 18-DEC-2003.
XX
XX 05-JUN-2003; 2003WO-GB002450.
XX
XX 05-JUN-2002; 2002GB-00012885.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Anderson RP, Hill AVS, Jewell DP;
XX
XX WPI; 2004-043640/04.
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.

PS Example 4; SEQ ID NO 11; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

CC Sequence 20 AA;

Query Match 100.0%; Score 97; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLOPFPQPELPYQPOS 17
 Db 2 QLOPFPQPELPYQPOS 18

RESULT 13

AAU01803 standard; protein; 17 AA.

AC AAU01803;
 DT 07-SEP-2001 (first entry)
 DE Wheat A-gliadin 57-73, E65, 72 mutant peptide.

KM Wheat; A-gliadin; E65, 72; coeliac disease; gluten intolerance;
 KM T-cell binding; antagonist; transglutaminase; transgenic plant; mutein.

OS Triticum aestivum.

PN WO200125793-A2.

PD 12-APR-2001.

PF 02-OCT-2000; 2000WO-GB003760.

PR 01-OCT-1999; 99GB-00023306.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2001-300179/31.

PT Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.

PS Disclosure; Page 4; 107pp; English.

CC The sequence represents wheat A-gliadin T-cell epitope E65, 72, which has
 CC Gln substituted with Glu at positions corresponding to 65 and 72 of the
 CC full length A-gliadin. The peptides of the invention are used to test
 CC mammalian (preferably human) susceptibility to coeliac disease (gluten
 CC intolerance). The peptides are contacted with a blood sample and T cell
 CC recognition measured, a positive T-cell recognition indicating a
 CC susceptibility to coeliac disease. The peptides are useful for inducing
 CC tolerance in an individual and antagonists to the peptides are useful for
 CC treating or preventing coeliac disease in an individual and for producing
 CC an antibody specific to them or a wild-type sequence. A mutant gliadin

CC protein (or its fragment of 15 amino acids in length) whose wild-type
 CC sequence can be modified by transglutaminase to a sequence that comprises
 CC the epitope, but which has been modified in such a way that it does not
 CC contain sequence which can be modified by transglutaminase to a sequence
 CC that comprise the epitope is useful for decreasing the ability of gliadin
 CC protein to cause Coeliac disease. Nucleic acids encoding proteins
 CC antagonistic to the T-cell binding of the epitopes are useful for
 CC obtaining a transgenic plant cell or seed and for the production of a
 CC protein. The resultant crop plant is useful for obtaining a product of a
 CC wheat plant, especially grain, which is optionally processed into flour
 CC or another grain product. Food comprising the antagonistic protein is
 CC useful instead of a wild-type gliadin

CC Sequence 17 AA;

Query Match 96.9%; Score 94; DB 4; Length 17;
 Best Local Similarity 94.1%; Pred. No. 2.6e-05;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QLOPFPQPELPYQPOS 17
 Db 1 QLOPFPQPELPYQPOS 17

RESULT 14

AAU01802 standard; protein; 17 AA.

AC AAU01802;
 DT 07-SEP-2001 (first entry)
 DE Wheat A-gliadin 57-73, E57, 65 mutant peptide.

KM Wheat; A-gliadin; E57, 65; coeliac disease; gluten intolerance;
 KM T-cell binding; antagonist; transglutaminase; transgenic plant; mutein.

OS Triticum aestivum.

PN WO200125793-A2.

PD 12-APR-2001.

PF 02-OCT-2000; 2000WO-GB003760.

PR 01-OCT-1999; 99GB-00023306.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2001-300179/31.

PT Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.

PS Disclosure; Page 4; 107pp; English.

CC The sequence represents wheat A-gliadin T-cell epitope E57, 65, which has
 CC Gln substituted with Glu at positions corresponding to 57 and 65 of the
 CC full length A-gliadin. The peptides of the invention are used to test
 CC mammalian (preferably human) susceptibility to coeliac disease (gluten
 CC intolerance). The peptides are contacted with a blood sample and T cell
 CC recognition measured, a positive T-cell recognition indicating a
 CC susceptibility to coeliac disease. The peptides are useful for inducing
 CC tolerance in an individual and antagonists to the peptides are useful for
 CC treating or preventing coeliac disease in an individual and for producing
 CC an antibody specific to them or a wild-type sequence. A mutant gliadin
 CC protein (or its fragment of 15 amino acids in length) whose wild-type
 CC sequence can be modified by transglutaminase to a sequence that comprises
 CC the epitope, but which has been modified in such a way that it does not

CC contain sequence which can be modified by transglutaminase to a sequence
 CC that comprise the epitope is useful for decreasing the ability of gliadin
 CC protein to cause Coeliac disease. Nucleic acids encoding proteins
 CC antagonistic to the T-cell binding of the epitopes are useful for
 CC obtaining a transgenic plant cell or seed and for the production of a
 CC protein. The resultant crop plant is useful for obtaining a product of a
 CC wheat plant, especially grain, which is optionally processed into flour
 CC or another grain product. Food comprising the antagonistic protein is
 CC useful instead of a wild-type gliadin

XX Sequence 17 AA;

CC Query Match

Best Local Similarity 94.1%; Score 94; DB 4; Length 17;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 QLPFPQPELPYPQPOS 17
 1 QLPFPQPELPYPQPOS 17

RESULT 15

AAU01806 standard; peptide; 17 AA.

AAU01806;

07-SEP-2001 (first entry)

Wheat A-gliadin 57-73 peptide.

Wheat; A-gliadin; 57-73 peptide; coeliac disease; gluten intolerance;

T-cell binding; antagonist; transglutaminase; transgenic plant.

Triticum aestivum.

WO200125793-A2.

12-APR-2001.

02-OCT-2000; 2000WO-GB003750.

01-OCT-1999; 99GB-00023306.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2001-300179/31.

Diagnosing coeliac disease or susceptibility to the disease in an
 individual, by detecting in vitro or in vivo T cells which bind
 immunodominant T cell epitope obtained from naturally occurring homolog
 of gliadin.

Example 1; Fig 12c; 107tp; English.

The sequence represents wheat A-gliadin 57-73 peptide. The peptides of
 the invention are used to test mammalian (preferably human)
 susceptibility to coeliac disease (gluten intolerance). The peptides are
 contacted with a blood sample and T cell recognition measured, a positive
 T-cell recognition indicating a susceptibility to coeliac disease. The
 peptides are useful for inducing tolerance in an individual and
 antagonists to the peptides are useful for treating or preventing coeliac
 disease in an individual and for producing an antibody specific to them
 or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
 amino acids in length) whose wild-type sequence can be modified by
 transglutaminase to a sequence that comprises the epitope, but which has
 been modified in such a way that it does not contain sequence which can
 be modified by transglutaminase to a sequence that comprises the epitope
 is useful for decreasing the ability of gliadin protein to cause Coeliac
 disease. Nucleic acids encoding proteins antagonistic to the T-cell
 binding of the epitopes are useful for obtaining a transgenic plant cell

CC or seed and for the production of a protein. The resultant crop plant is
 CC useful for obtaining a product of a wheat plant, especially grain, which
 CC is optionally processed into flour or another grain product. Food
 CC comprising the antagonistic protein is useful instead of a wild-type
 CC gliadin

XX Sequence 17 AA;

CC Query Match

Best Local Similarity 94.1%; Score 94; DB 4; Length 17;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 QLPFPQPELPYPQPOS 17
 1 QLPFPQPELPYPQPOS 17

Search completed: December 14, 2004, 16:59:56
 Job time : 162.5 secs

PI Khosla C, Hausch F, Parrot I, Shan L;
 XX WPI; 2004-098857/10.
 DR
 XX
 XX Method useful for treatment of celiac sprue and/or dermatitis
 PT herpeticiformis involves the use of tissue transglutaminase (tTGase)
 PR inhibitor to attenuate gluten toxicity.
 XX
 XX Disclosure; Page 8; 37pp; English.
 XX
 XX The invention relates to a method for the treatment of celiac sprue
 CC and/or dermatitis herpeticiformis, involving the administration of tissue
 CC transglutaminase (tTGase) inhibitor to attenuate gluten toxicity in the
 CC patient. The method of the invention is useful for the treatment of
 CC celiac sprue and dermatitis herpeticiformis, or for the treatment of a
 CC disorder where tissue transglutaminase is a factor in disease etiology,
 CC such as a neurological disorder, cancer or wound healing. The method of
 CC the invention is also useful in the treatment of progressive supranuclear
 CC palsy, Huntington's, Alzheimer's and Parkinson's diseases, the aberrant
 CC activation of Tgases may be caused by oxidative stress and inflammation.
 CC The formulation reduces the toxic effects of toxic gluten oligopeptides,
 CC thus attenuating or eliminates the damaging effects of gluten. The
 CC formulation allows the celiac sprue individual to eat gluten-containing
 CC foodstuffs without ill effect, or at least to tolerate such foodstuffs in
 CC small or moderate quantities without inducing relapse. The current
 CC sequence represents a high affinity peptide substrate for tTGase that
 CC acts as a glutenase resistant peptide.
 CC
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 42; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 1 POPELPY 7
 Db 1 POPELPY 7
 RESULT 4
 ADH14511
 ID ADH14511 standard; peptide; 7 AA.
 XX
 XX ADH14511;
 AC
 XX
 XX 11-MAR-2004 (first entry)
 DT
 XX
 XX Gliadin related epitope peptide SEQ ID NO:1.
 DE
 XX
 XX celiac disease; gliadin, gliadin T cell epitope; gastrointestinal;
 KW vaccine.
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003104273-A2.
 PN
 XX
 XX 18-DEC-2003.
 PD
 XX
 XX 05-JUN-2003; 2003WO-GE002450.
 PF
 XX
 XX 05-JUN-2002; 2002GB-00012885.
 PR
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA
 XX
 XX Anderson RP, Hill AVS, Jewell DP;
 PI
 XX
 XX WPI; 2004-043640/04.
 DR
 XX
 XX Preventing or treating celiac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 CC cell receptor.
 CC
 XX Claim 1; SEQ ID NO 1; 177bp; English.
 PS

best data

XX
 CC The present invention describes a method (M1) for preventing or treating
 CC celiac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognized by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC celiac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing celiac disease, or susceptibility to celiac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, celiac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 CC
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 42; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0;
 QY 1 POPELPY 7
 Db 1 POPELPY 7
 RESULT 5
 ADF91460
 ID ADF91460 standard; peptide; 9 AA.
 XX
 XX ADF91460;
 AC
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX
 XX T-cell epitope peptide.
 DE
 XX
 XX Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
 KW gluten; Celiac Sprue; dermatitis herpeticiformis; HLA-DQ2 positive;
 KW type I diabetes; protein co-ordinate data.
 XX
 XX Synthetic.
 OS
 XX
 XX WO2003096984-A2.
 PN
 XX
 XX 27-NOV-2003.
 PD
 XX
 XX 14-MAY-2003; 2003WO-US015506.
 PF
 XX
 XX 14-MAY-2002; 2002US-0380761P.
 PR
 XX
 XX 28-JUN-2002; 2002US-0392782P.
 PR
 XX
 XX 31-OCT-2002; 2002US-0422933P.
 PR
 XX
 XX 20-NOV-2002; 2002US-0428033P.
 XX
 XX (STRD) UNIV IRLAND STANFORD JUNIOR.
 PA
 XX
 XX (SOLDL) SOLID L M.
 PA
 XX
 XX (HAUS/) HAUSCH F.
 PA
 XX
 XX (SHAN/) SHAN L.
 PA
 XX
 XX (KHOS/) KHOSLA C.
 PA
 XX
 XX (QUAR/) QUARSTEN H.
 PI
 XX
 XX Solid LM, Hausch F, Shan L, Khosla C, Quarsten H, Gray G;
 PI
 XX
 XX Kim C;
 DR
 XX
 XX WPI; 2004-053078/05.
 DR
 XX
 XX New HLA-binding peptide inhibitor that is an analog of an immunogenic
 PT gluten oligopeptide, useful for preparing a composition for treating
 PT e.g., Celiac Sprue or dermatitis herpeticiformis.
 XX
 XX Claim 5; Page 112; 115pp; English.
 CC
 CC The invention relates to a new HLA-binding peptide inhibitor, which is an
 CC analog of an immunogenic gluten oligopeptide of at least about 8 residues

best data

CC in length, altered by the replacement of one or more amino acids and that
 CC binds tightly to HLA molecules, and is proteolytically stable and does
 CC not activate disease-specific T cells. Also disclosed is a computer for
 CC producing a three-dimensional representation of an HLA-DQ2 molecule bound
 CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
 CC comprises the sequence PXPPELPY. The HLA-binding peptide inhibitor is
 CC useful for preparing a composition for treating Celiac Sprue or
 CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
 CC predisposed to or have developed symptoms of type I diabetes. The current
 CC sequence represents an immunogenic gluten oligopeptide fragment that may
 CC be modified to generate an HLA-binding peptide inhibitor. This particular
 CC peptide represents a T-cell epitope that forms part of the 33-mer
 CC immunogenic gluten peptide given in ADF91457.

SC Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PXPPELPY 7
 |||||
 DB 3 PXPPELPY 9

RESULT 6

ADFP91462
 ID ADF91462 standard; peptide; 9 AA.

AC ADF91462;

DT 26-FEB-2004 (first entry)

DE T-cell epitope peptide.

KW Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
 KW gluten; Celiac Sprue; dermatitis herpetiformis; HLA-DQ2 positive;

KM type I diabetes; protein co-ordinate data.

OS Synthetic.

PN WO2003096984-A2.

PD 27-NOV-2003.

PE 14-MAY-2003; 2003WO-US015506.

PR 14-MAY-2002; 2002US-0380761P.

PR 28-JUN-2002; 2002US-0392782P.

PR 31-OCT-2002; 2002US-0422933P.

PR 20-NOV-2002; 2002US-0428033P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PA (SOLU/) SOLID L M.

PA (HAUS/) HAUSCH F.

PA (SHAN/) SHAN L.

PA (KHOS/) KHOSIA C.

PA (QUAR/) QUARSTEN H.

PI SOLID LM, Hausch F, Shan L, Khosia C, Quarsten H, Gray G;

PI Kim C;

PI WPI; 2004-053078/05.

PT New HLA-binding peptide inhibitor that is an analog of an immunogenic
 PT gluten oligopeptide, useful for preparing a composition for treating
 PT e.g., Celiac Sprue or dermatitis herpetiformis.

PS Claim 5; Page 112; 115pp; English.

CC The invention relates to a new HLA-binding peptide inhibitor, which is an
 CC analog of an immunogenic gluten oligopeptide of at least about 8 residues
 CC in length, altered by the replacement of one or more amino acids and that

CC binds tightly to HLA molecules, and is proteolytically stable and does
 CC not activate disease-specific T cells. Also disclosed is a computer for
 CC producing a three-dimensional representation of an HLA-DQ2 molecule bound
 CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
 CC comprises the sequence PXPPELPY. The HLA-binding peptide inhibitor is
 CC useful for preparing a composition for treating Celiac Sprue or
 CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
 CC predisposed to or have developed symptoms of type I diabetes. The current
 CC sequence represents an immunogenic gluten oligopeptide fragment that may
 CC be modified to generate an HLA-binding peptide inhibitor. This particular
 CC peptide represents a T-cell epitope that forms part of the 33-mer
 CC immunogenic gluten peptide given in ADF91457.

SC Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PXPPELPY 7
 |||||
 DB 3 PXPPELPY 9

RESULT 7

ADFP91464
 ID ADF91464 standard; peptide; 9 AA.

AC ADF91464;

DT 26-FEB-2004 (first entry)

DE Immunogenic gluten oligopeptide.

KW Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
 KW gluten; Celiac Sprue; dermatitis herpetiformis; HLA-DQ2 positive;

KM type I diabetes; protein co-ordinate data.

OS Synthetic.

PN WO2003096984-A2.

PD 27-NOV-2003.

PE 14-MAY-2003; 2003WO-US015506.

PR 14-MAY-2002; 2002US-0380761P.

PR 28-JUN-2002; 2002US-0392782P.

PR 31-OCT-2002; 2002US-0422933P.

PR 20-NOV-2002; 2002US-0428033P.

PA (STRD) UNIV LELAND STANFORD JUNIOR.

PA (SOLU/) SOLID L M.

PA (HAUS/) HAUSCH F.

PA (SHAN/) SHAN L.

PA (KHOS/) KHOSIA C.

PA (QUAR/) QUARSTEN H.

PI SOLID LM, Hausch F, Shan L, Khosia C, Quarsten H, Gray G;

PI Kim C;

PI WPI; 2004-053078/05.

PT New HLA-binding peptide inhibitor that is an analog of an immunogenic
 PT gluten oligopeptide, useful for preparing a composition for treating
 PT e.g., Celiac Sprue or dermatitis herpetiformis.

best data

best data

Location/Qualifiers
 2
 /note= "X is Tyr, Trp, Arg, Lys, p-Iodo-Phe, p-Iodo-Tyr,
 P-amino-Phe, 3-amino-Tyr, hydroxylysine, ornithine, Asp,
 Glu"

PS Claim 6; Page 112; 115pp; English.
CC The invention relates to a new HLA-binding peptide inhibitor, which is an
CC analog of an immunogenic gluten oligopeptide of at least about 8 residues
CC in length, altered by the replacement of one or more amino acids and that
CC binds tightly to HLA molecules, and is proteolytically stable and does
CC not activate disease-specific T cells. Also disclosed is a computer for
CC producing a three-dimensional representation of an HLA-DQ2 molecule bound
CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
CC comprises the sequence PQLPELPY. The HLA-binding peptide inhibitor is
CC useful for preparing a composition for treating Celiac Sprue or
CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
CC predisposed to or have developed symptoms of type I diabetes. The current
CC sequence represents an immunogenic gluten oligopeptide that may be
CC modified to generate an HLA-binding peptide inhibitor.

SQ Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 PQLPELPY 7
|||
Db 3 PQLPELPY 9

RESULT 8
ADP91461
ID ADP91461 standard; peptide; 9 AA.

XX ADP91461;

XX 26-FEB-2004 (first entry)

XX T-cell epitope peptide.

XX Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
XX gluten; Celiac Sprue; dermatitis herpetiformis; HLA-DQ2 positive;
XX type I diabetes; protein co-ordinate data.

OS Synthetic.

XX WO2003096984-A2.

XX 27-NOV-2003.

XX 14-MAY-2003; 2003WO-US015506.

XX 14-MAY-2002; 2002US-0380761P.

XX 28-JUN-2002; 2002US-0392782P.

XX 31-OCT-2002; 2002US-0422933P.

XX 20-NOV-2002; 2002US-0428033P.

best data

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX (SOLL) SOLID L M.

XX (HAUS) HAUSCH F.

XX (SHAN) SHAN L. C.

XX (KHOS) KHOSLA C.

XX (QUAR) QUARSTEN H.

XX Solid LM, Hausch F, Shan L, Khosla C, Quarsten H, Gray G;

XX Kim C;

XX WPI, 2004-053078/05.

XX New HLA-binding peptide inhibitor that is an analog of an immunogenic
XX gluten oligopeptide, useful for preparing a composition for treating
XX e.g., Celiac Sprue or dermatitis herpetiformis.
XX Disclosure; Page 7; 115pp; English.
XX The invention relates to a new HLA-binding peptide inhibitor, which is an

CC analog of an immunogenic gluten oligopeptide of at least about 8 residues
CC in length, altered by the replacement of one or more amino acids and that
CC binds tightly to HLA molecules, and is proteolytically stable and does
CC not activate disease-specific T cells. Also disclosed is a computer for
CC producing a three-dimensional representation of an HLA-DQ2 molecule bound
CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
CC comprises the sequence PQLPELPY. The HLA-binding peptide inhibitor is
CC useful for preparing a composition for treating Celiac Sprue or
CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
CC predisposed to or have developed symptoms of type I diabetes. The current
CC sequence represents an immunogenic gluten oligopeptide fragment that may
CC be modified to generate an HLA-binding peptide inhibitor. This particular
CC immunogenic gluten peptide given in ADP91457.

SQ Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Gaps 0;

Qy 1 PQLPELPY 7
|||
Db 1 PQLPELPY 7

RESULT 9
ADP19619
ID ADP19619 standard; peptide; 9 AA.

XX ADP19619;

XX 26-AUG-2004 (first entry)

XX Antigenic gluten oligopeptide epitope, SEQ ID 21.

XX Gluten; Celiac Sprue; wheat.

XX Triticum aestivum.

XX WO2004045392-A2.

XX 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037434.

XX 20-NOV-2002; 2002US-0428033P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Khosla C, Shan L;

XX WPI, 2004-460460/43.

XX New gluten oligopeptides, useful for diagnosing Celiac Sprue, in
XX diagnostic assays for detecting antibodies against such oligopeptides, or
XX for producing antibodies that bind specifically to such oligopeptides.

XX Claim 2; SEQ ID NO 21; 50pp; English.

XX The present invention relates to novel purified gluten oligopeptides. The

XX gluten oligopeptides comprise multiple T cell or B cell epitopes

XX (ADP19608, ADP19616-ADP19623). The gluten oligopeptides are useful in

XX stimulating T cells from Celiac Sprue patients for diagnostic purposes,

XX in diagnostic assays for detecting antibodies against such oligopeptides,

XX or for producing antibodies that bind specifically to such oligopeptides.

XX Sequence 9 AA;

Query Match 100.0%; Score 42; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Gaps 0;
Matches 7; Conservative 0; Indels 0; Gaps 0;

QY 1 POPELRY 7
 DB 1 POPELRY 7

RESULT 10

ADP19623

ADP19623 standard; peptide; 9 AA.

XX ADP19623;

XX 26-AUG-2004 (first entry)

XX Antigenic gluten oligopeptide epitope, SEQ ID 25.

XX Gluten; Celiac Sprue; wheat.

XX Triticum aestivum.

XX WO2004045392-A2.

XX 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037434.

XX 20-NOV-2002; 2002US-0428033P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Khosla C, Shan L;

XX WPI; 2004-460460/43.

XX New gluten oligopeptides, useful for diagnosing Celiac Sprue, in
 XX diagnostic assays for detecting antibodies against such oligopeptides, or
 XX for producing antibodies that bind specifically to such oligopeptides.

XX Claim 2; SEQ ID NO 25; 50bp; English.

XX The present invention relates to novel purified gluten oligopeptides. The
 XX gluten oligopeptides comprise multiple T cell or B cell epitopes
 XX (ADP19608, ADP19616-ADP19623). The gluten oligopeptides are useful in
 XX stimulating T cells from Celiac Sprue patients for diagnostic purposes,
 XX in diagnostic assays for detecting antibodies against such oligopeptides,
 XX or for producing antibodies that bind specifically to such oligopeptides.

XX Sequence 9 AA;

XX Query Match Best Local Similarity 100.0%; Score 42; DB 8; Length 9;

XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

ADP19620

ADP19620 standard; peptide; 9 AA.

XX ADP19620;

XX 26-AUG-2004 (first entry)

XX Antigenic gluten oligopeptide epitope, SEQ ID 22.

XX Gluten; Celiac Sprue; wheat.

XX Triticum aestivum.

XX WO2004045392-A2.

XX

XX

XX

XX

XX

PD 03-JUN-2004.

XX 20-NOV-2003; 2003WO-US037434.

XX 20-NOV-2002; 2002US-0428033P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Khosla C, Shan L;

XX WPI; 2004-460460/43.

XX New gluten oligopeptides, useful for diagnosing Celiac Sprue, in
 XX diagnostic assays for detecting antibodies against such oligopeptides, or
 XX for producing antibodies that bind specifically to such oligopeptides.

XX Claim 2; SEQ ID NO 22; 50bp; English.

XX The present invention relates to novel purified gluten oligopeptides. The
 XX gluten oligopeptides comprise multiple T cell or B cell epitopes
 XX (ADP19608, ADP19616-ADP19623). The gluten oligopeptides are useful in
 XX stimulating T cells from Celiac Sprue patients for diagnostic purposes,
 XX in diagnostic assays for detecting antibodies against such oligopeptides,
 XX or for producing antibodies that bind specifically to such oligopeptides.

XX Sequence 9 AA;

XX Query Match Best Local Similarity 100.0%; Score 42; DB 8; Length 9;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX

XX

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XX

DR WPI; 2004-053078/05.
XX New HLA-binding peptide inhibitor that is an analog of an immunogenic
PT gluten oligopeptide, useful for preparing a composition for treating
PT e.g., Celiac Sprue or dermatitis herpetiformis.
XX
XX Claim 5; Page 112; 115pp; English.
CC The invention relates to a new HLA-binding peptide inhibitor, which is an
CC analog of an immunogenic gluten oligopeptide of at least about 8 residues
CC in length, altered by the replacement of one or more amino acids and that
CC binds tightly to HLA molecules, and is proteolytically stable and does
CC not activate disease-specific T cells. Also disclosed is a computer for
CC producing a three-dimensional representation of an HLA-DQ2 molecule bound
CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
CC comprises the sequence PPELPY 7. The HLA-binding peptide inhibitor is
CC useful for preparing a composition for treating Celiac Sprue or
CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
CC predisposed to or have developed symptoms of type 1 diabetes. The current
CC sequence represents an immunogenic gluten oligopeptide that may be
CC modified to generate an HLA-binding peptide inhibitor.
SQ Sequence 10 AA;

Query Match 100.0%; Score 42; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PPELPY 7
|||
3 PPELPY 9

Db

RESULT 13
AAU01811
ID AAU01811 standard; peptide; 11 AA.
XX
XX AAU01811;
XX
XX 07-SEP-2001 (first entry)
XX
XX
XX Wheat A-gliadin 57-73 Q65 bioactive residues.
XX
XX
XX Wheat; A-gliadin; immunodominant T-cell epitope; coeliac disease;
XX gluten intolerance; T-cell binding; antagonist; transglutaminase;
XX transgenic plant; A-gliadin 57-73 Q65.
XX
XX Triticum aestivum.
XX
XX WO200125793-A2.
XX
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-GB003760.
XX
XX 01-OCT-1999; 99GB-00023306.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Anderson RP, Hill AVS, Jewell DP;
XX
XX WPI; 2001-300179/31.
XX
XX
XX Diagnosing coeliac disease or susceptibility to the disease in an
XX individual, by detecting in vitro or in vivo T cells which bind
XX immunodominant T cell epitope obtained from naturally occurring homolog
XX of gliadin.
XX
XX Example 9; Page 45; 107pp; English.
XX
XX The sequence represents residues 4-17 of wheat A-gliadin immunodominant T
XX cell epitope, A-gliadin 57-73 Q65 (where the Gln at a position
XX corresponding to 65 in the full length A-gliadin has been converted to a

CC glu by the action of a transglutaminase), found to contribute
CC substantially to the bioactivity of A-gliadin 57-73 Q65. The peptides of
CC the invention are used to test mammalian (preferably human)
CC susceptibility to coeliac disease (gluten intolerance). The peptides are
CC contacted with a blood sample and T-cell recognition measured, a positive
CC T-cell recognition indicating a susceptibility to coeliac disease. The
CC peptides are useful for inducing tolerance in an individual and
CC antagonists to the peptides are useful for treating or preventing coeliac
CC disease in an individual and for producing an antibody specific to them
CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
CC amino acids in length) whose wild-type sequence can be modified by
CC transglutaminase to a sequence that comprises the epitope, but which has
CC been modified in such a way that it does not contain sequence which can
CC be modified by transglutaminase to a sequence that comprise the epitope
CC is useful for decreasing the ability of gliadin protein to cause Coeliac
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
CC binding of the epitopes are useful for obtaining a transgenic plant cell
CC or seed and for the production of a protein. The resultant crop plant is
CC useful for obtaining a product of a wheat plant, especially grain, which
CC is optionally processed into flour or another grain product. Food
CC comprising the antagonistic protein is useful instead of a wild-type
CC gliadin
SQ Sequence 11 AA;

Query Match 100.0%; Score 42; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PPELPY 7
|||
3 PPELPY 9

Db

RESULT 14
ADH14524
ID ADH14524 standard; peptide; 11 AA.
XX
XX ADH14524;
XX
XX 11-MAR-2004 (first entry)
XX
XX
XX Gliadin related epitope peptide SEQ ID NO:14.
XX
XX
XX Coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
XX vaccine.
XX
XX Synthetic.
XX
XX WO2003104273-A2.
XX
XX 18-DEC-2003.
XX
XX 05-JUN-2003; 2003WO-GB002450.
XX
XX 05-JUN-2002; 2002GB-00012885.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Anderson RP, Hill AVS, Jewell DP;
XX
XX WPI; 2004-043640/04.
XX
XX
XX Preventing or treating coeliac disease comprises administering agent
XX which are wheat gliadin T cell epitope capable of being recognized by T
XX cell receptor.
XX
XX Example 9; SEQ ID NO 14; 177pp; English.
XX
XX The present invention describes a method (M1) for preventing or treating
XX coeliac disease. M1 comprises administering an agent (A) comprising a
XX gliadin T cell epitope, which is capable of being recognised by a T cell
XX receptor, to an individual. Gliadin is a component of gluten. (A) has

CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.

SC Sequence 11 AA:

Query Match Best Local Similarity 100.0%; Score 42; DB 8; Length 11;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGPRLPY 7
| | | | |
DQ 3 PGPRLPY 9

RESULT 15

ADH14655
ADH14655 standard; peptide; 11 AA.

AG ADH14655;

DE 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KM vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PE 05-JUN-2003; 2003WO-GB002450.

PE 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PL Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.

PS Example 6; Page 80; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.

SC Sequence 11 AA:

Query Match Best Local Similarity 100.0%; Score 42; DB 8; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.9; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY 1 PGPRLPY 7
| | | | |
DQ 5 PGPRLPY 11

RESULT 16

AAU01827
AAU01827 standard; peptide; 12 AA.

AC AAU01827;

DT 07-SEP-2001 (first entry)

DE Alpha-gliadin T-cell epitope described in coeliac disease #1.

KM wheat; alpha-gliadin; T-cell epitope; coeliac disease;

KM gluten intolerance; antagonist; transglutaminase; transgenic plant.

OS Triticum aestivum.

PN WO200125793-A2.

PD 12-APR-2001.

PE 02-OCT-2000; 2000WO-GB003760.

PE 01-OCT-1999; 99GB-00023306.

PA (ISIS-) ISIS INNOVATION LTD.

PL Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2001-300179/31.

PT Diagnosing coeliac disease or susceptibility to the disease in an
PT individual, by detecting in vitro or in vivo T cells which bind
PT immunodominant T cell epitope obtained from naturally occurring homolog
PT of gliadin.

PS Example 6; Fig 12e; 107pp; English.

CC The sequence is a wheat alpha-gliadin T-cell epitope described in coeliac
CC disease. The peptides of the invention are used to test mammalian
CC (preferably human) susceptibility to coeliac disease (gluten
CC intolerance). The peptides are contacted with a blood sample and T cell
CC recognition measured a positive T-cell recognition indicating a
CC susceptibility to coeliac disease. The peptides are useful for inducing
CC tolerance in an individual and antagonists to the peptides are useful for
CC treating or preventing coeliac disease in an individual and for producing
CC an antibody specific to them or a wild-type sequence. A mutant gliadin
CC protein (or its fragment of 15 amino acids in length) whose wild-type
CC sequence can be modified by transglutaminase to a sequence that comprises
CC the epitope, but which has been modified in such a way that it does not
CC contain sequence which can be modified by transglutaminase to a sequence
CC that comprises the epitope is useful for decreasing the ability of gliadin
CC protein to cause Coeliac disease. Nucleic acids encoding proteins
CC antagonistic to the T-cell binding of the epitopes are useful for
CC obtaining a transgenic plant cell or seed and for the production of a
CC protein. The resultant crop plant is useful for obtaining a product of a
CC wheat plant, especially grain, which is optionally processed into flour
CC or another grain product. Food comprising the antagonistic protein is
CC useful instead of a wild-type gliadin

SC Sequence 12 AA:

Query Match Best Local Similarity 100.0%; Score 42; DB 4; Length 12;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PGPRLPY 7

Db 6 POPELPY 12

RESULT 17
AAU01809 standard; peptide; 12 AA.

07-SEP-2001 (first entry)

Wheat alpha9-gliadin chymotrypsin digest peptide.

Wheat; A-gliadin; chymotrypsin digest peptide; coeliac disease;
gluten intolerance; T-cell binding; antagonist; transglutaminase;
transgenic plant; alpha9-gliadin.

Triticum aestivum.

WO200125793-A2.

12-APR-2001.

02-OCT-2000; 2000WO-GB003760.

01-OCT-1999; 99GB-00023306.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2001-300179/31.

Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.

Example 7; Page 42; 107pp; English.

The sequence represents a peptide released by chymotryptic digestion of recombinant alpha9-gliadin, representing a truncation of the optimal epitope sequence (presented as AAU01798) The peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can be modified by transglutaminase to a sequence that comprise the epitope is useful for decreasing the ability of gliadin protein to cause Coeliac disease. Nucleic acids encoding proteins antagonistic to the T-cell binding of the epitopes are useful for obtaining a transgenic plant cell or seed and for the production of a protein. The resultant crop plant is useful for obtaining a product of a wheat plant, especially grain, which is optionally processed into flour or another grain product. Food comprising the antagonistic protein is useful instead of a wild-type gliadin

Sequence 12 AA:

Query Match 100.0%; Score 42; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
DB 6 POPELPY 12

RESULT 18
AAE38560 standard; peptide; 12 AA.

04-DEC-2003 (first entry)

Wheat peptide #2 used to illustrate the method of the invention.

Wheat; therapy; celiac sprue; dermatitis herpetiformis; gluten toxicity;
glutenase; foodstuff; antiinflammatory; dermatological.

Triticum aestivum.

WO2003068170-A2.

21-AUG-2003.

14-FEB-2003; 2003WO-US004743.

14-FEB-2002; 2002US-0357238P.

14-MAY-2002; 2002US-0380761P.

28-JUN-2002; 2002US-0392782P.

31-OCT-2002; 2002US-0422933P.

20-NOV-2002; 2002US-0428033P.

20-DEC-2002; 2002US-0435881P.

(STRD) UNIV LEBLAND STANFORD JUNIOR.

Hausch F, Gray G, Shan L, Khosla C;

WPI; 2003-697466/66.

Treating celiac sprue and/or dermatitis herpetiformis comprises administering to a patient a dose of a glutenase that attenuates gluten toxicity in the patient.

Claim 4; Page 52; 69pp; English.

The present invention relates to a method for treating celiac sprue and/or dermatitis herpetiformis. The method involves administering to a patient a dose of a glutenase that attenuates gluten toxicity in the patient. The method is also useful in treating a foodstuff to render the foodstuff less toxic to a celiac sprue patient. The present sequence is a wheat peptide used to illustrate the method of the invention

Sequence 12 AA:

Query Match 100.0%; Score 42; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
DB 6 POPELPY 12

RESULT 19
ADP91475 standard; peptide; 12 AA.

ADP91475;

26-FEB-2004 (first entry)

Peptide fused to HLA-DQ2 beta chain.

Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
gluten; celiac sprue; dermatitis herpetiformis; HLA-DQ2 positive;
type I diabetes; protein co-ordinate data.

*unpublished
to patent*

first entry

Synthetic.

WO2003096984-A2.

27-NOV-2003.

14-MAY-2003; 2003WO-US015506.

14-MAY-2003; 2002US-0380761P.

28-JUN-2002; 2002US-0392782P.

31-OCT-2002; 2002US-0422933P.

20-NOV-2002; 2002US-0428033P.

(STRD) UNIV IELAND STANFORD JUNIOR.

(SOLL) SOLID L. M.

(HAUS) HAUSCH F.

(SHAN) SHAN L.

(KHOS) KHOSLA C.

(QVAR) QVARSTEN H.

Solid IM, Hausch F, Shan L, Khosla C, Quarsten H, Gray G;

Kim C;

WPI; 2004-053078/05.

New HLA-binding peptide inhibitor that is an analog of an immunogenic

gluten oligopeptide, useful for preparing a composition for treating

e.g., Celiac Sprue or dermatitis herpetiformis.

Example 3; Page 22; 115pp; English.

The invention relates to a new HLA-binding peptide inhibitor, which is an

analog of an immunogenic gluten oligopeptide of at least about 8 residues

in length, altered by the replacement of one or more amino acids and that

binds tightly to HLA molecules, and is proteolytically stable and does

not activate disease-specific T cells. Also disclosed is a computer for

producing a three-dimensional representation of an HLA-DQ2 molecule bound

to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor

comprises the sequence PQLPELPY 7

useful for preparing a composition for treating Celiac Sprue or

dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either

predisposed to or have developed symptoms of type 1 diabetes. The current

sequence represents a peptide that is fused to the beta-chain of HLA-DQ2

in an example from the invention, for the purposes of X-ray

crystallographic analysis of soluble HLA-DQ2.

Sequence 12 AA;

Query Match

Best Local Similarity

Matches

7; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

0;

0;

0;

0;

RESULT 20

ADH14576

AC ADH14576;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

XX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

XX Example 14; Page 71; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating

CC coeliac disease. M1 comprises administering an agent (A) comprising a

CC gliadin T cell epitope, which is capable of being recognised by a T cell

CC receptor, to an individual. Gliadin is a component of gluten. (A) has

CC gastrointestinal activity, and can be used in vaccines. The agent (A) can

CC be used in the preparation of a medicament for treating or preventing

CC coeliac disease. (A) can also be used in the preparation of a diagnostic

CC means for use in diagnosing coeliac disease, or susceptibility to coeliac

CC disease, in an individual, which involves determining whether T cells of

CC the individual recognise the agent, recognition by the T cells indicating

CC that the individual has, or is susceptible to, coeliac disease. The

CC present sequence represents a peptide which is used in the

CC exemplification of the present invention.

XX Sequence 12 AA;

Query Match

Best Local Similarity

Matches

7; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

0;

0;

0;

RESULT 21

ADH14559

AC ADH14559;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

XX vaccine.

OS Synthetic.

XX WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX Example 14; Page 66; 177pp; English.
XX
CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
CC
SQ Sequence 12 AA;
XX
CC Query Match 100.0%; Score 42; DB 8; Length 12;
CC Best Local Similarity 100.0%; Pred. No. 2.1;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 POPELPY 7
XX |||||
DB 6 POPELPY 12
XX
RESULT 22
ADH14573
ID ADH14573 standard; peptide; 12 AA.
XX
XX
XX ADH14573;
AC
XX 11-MAR-2004 (first entry)
DT
XX Gliadin related epitope peptide.
DE
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
OS Synthetic.
XX
XX WO2003104273-A2.
PN
XX 18-DEC-2003.
PD
XX
XX 05-JUN-2003; 2003WO-GB002450.
PF
XX
XX 05-JUN-2002; 2002GB-00012885.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX Anderson RP, Hill AVS, Jewell DP;
PI
XX WPI; 2004-043640/04.
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX Example 14; Page 71; 177pp; English.
XX
CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
CC
SQ Sequence 12 AA;
XX
CC Query Match 100.0%; Score 42; DB 8; Length 12;
CC Best Local Similarity 100.0%; Pred. No. 2.1;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
CC
SQ Sequence 12 AA;
XX
CC Query Match 100.0%; Score 42; DB 8; Length 12;
CC Best Local Similarity 100.0%; Pred. No. 2.1;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 POPELPY 7
XX |||||
DB 6 POPELPY 12
XX
RESULT 23
ADH16186
ID ADH16186 standard; peptide; 12 AA.
XX
XX
XX ADH16186;
AC
XX 11-MAR-2004 (first entry)
DT
XX Gliadin related epitope peptide.
DE
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
XX Synthetic.
XX
XX WO2003104273-A2.
PN
XX 18-DEC-2003.
PD
XX
XX 05-JUN-2003; 2003WO-GB002450.
PF
XX
XX 05-JUN-2002; 2002GB-00012885.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX Anderson RP, Hill AVS, Jewell DP;
PI
XX WPI; 2004-043640/04.
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX Example 6; Fig 12e; 177pp; English.
XX
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
CC
SQ Sequence 12 AA;
XX
CC Query Match 100.0%; Score 42; DB 8; Length 12;
CC Best Local Similarity 100.0%; Pred. No. 2.1;
CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX

OY 1 POPELPHY 7
 DB 6 POPELPHY 12

RESULT 24

ADH14523
 ID ADH14523 standard; peptide; 12 AA.

AC ADH14523;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide SEQ ID NO:13.

DM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KM vaccine.

OS Synthetic.

EN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012865.

PS (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

PS Example 7; SEQ ID NO 13; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

SQ Sequence 12 AA;

Query Match 100.0%; Score 42; DB 8; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPHY 7
 DB 6 POPELPHY 12

RESULT 25

ADH14571
 ID ADH14571 standard; peptide; 12 AA.

AC ADH14571;

DT 11-MAR-2004 (first entry)

XX Gliadin related epitope peptide.

DM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KM vaccine.

OS Synthetic.

EN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012865.

PS (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PT cell receptor.

PS Example 14; Page 71; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

SQ Sequence 12 AA;

Query Match 100.0%; Score 42; DB 8; Length 12;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPHY 7
 DB 6 POPELPHY 12

RESULT 26

ADH14648
 ID ADH14648 standard; peptide; 12 AA.

AC ADH14648;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

DM coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KM vaccine.

OS Synthetic.

EN WO2003104273-A2.

PD 18-DEC-2003.

PR 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.
 PR (ISIS-) ISIS INNOVATION LTD.
 PA
 PI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI: 2004-043640/04.
 XX
 PT Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.
 XX
 PS Example 6; Page 80; 177pp; English.
 XX
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 XX
 SQ Sequence 12 AA;
 XX
 Query Match 100.0%; Score 42; DB 8; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 POPELPY 7
 Db 6 POPELPY 12
 XX
 RESULT 27
 AAE38563
 ID AAE38563 standard; peptide; 13 AA.
 XX
 AC AAE38563;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Wheat peptide #5 used to illustrate the method of the invention.
 XX
 KM Wheat; therapy; celiac sprue; dermatitis herpetiformis; gluten toxicity;
 KM glutenase; foodstuff; antiinflammatory; dermatological.
 XX
 OS Triticum aestivum.
 XX
 PN WO2003068170-A2.
 PD 21-AUG-2003.
 XX
 PF 14-FEB-2003; 2003WO-US004743.
 XX
 PR 14-FEB-2002; 2002US-0357238P.
 PR 14-MAY-2002; 2002US-0380761P.
 PR 28-JUN-2002; 2002US-0392782P.
 PR 31-OCT-2002; 2002US-0422833P.
 PR 20-NOV-2002; 2002US-0428033P.
 PR 20-DEC-2002; 2002US-0435881P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Hauech F, Gray G, Shan L, Khosla C;
 XX
 DR WPI: 2003-697466/66.

best dates

XX Treating celiac sprue and/or dermatitis herpetiformis comprises
 PT administering to a patient a dose of a glutenase that attenuates gluten
 PT toxicity in the patient.
 XX
 PS Claim 2; Page 52; 69pp; English.
 XX
 CC The present invention relates to a method for treating celiac sprue
 CC and/or dermatitis herpetiformis. The method involves administering to a
 CC patient a dose of a glutenase that attenuates gluten toxicity in the
 CC patient. The method is also useful in treating a foodstuff to render the
 CC foodstuff less toxic to a celiac sprue patient. The present sequence is a
 CC wheat peptide used to illustrate the method of the invention
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 42; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 POPELPY 7
 Db 1 POPELPY 7
 XX
 RESULT 28
 ADF91447
 ID ADF91447 standard; peptide; 13 AA.
 XX
 AC ADF91447;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Immunogenic gluten oligopeptide.
 XX
 KM Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
 KM gluten; Celiac Sprue; dermatitis herpetiformis; HLA-DQ2 positive;
 KM type I diabetes; protein co-ordinate data.
 XX
 OS Synthetic.
 XX
 PN WO2003096984-A2.
 PD 27-NOV-2003.
 XX
 PF 14-MAY-2003; 2003WO-US015506.
 XX
 PR 14-MAY-2002; 2002US-0380761P.
 PR 28-JUN-2002; 2002US-0392782P.
 PR 31-OCT-2002; 2002US-0422833P.
 PR 20-NOV-2002; 2002US-0428033P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (SOL/L) SOL/LID L M.
 PA (HAUS/) HAUSCH F.
 PA (SHAN/) SHAN L.
 PA (KHOS/) KHOSLA C.
 PA (QUAR/) QUARSTEN H.
 XX
 PI SOL/LID LM, Hauech F, Shan L, Khosla C, Quarsten H, Gray G,
 PI Kim C;
 XX
 DR WPI: 2004-053078/05.
 XX
 PR New HLA-binding peptide inhibitor that is an analog of an immunogenic
 PR gluten oligopeptide, useful for preparing a composition for treating
 PR e.g., Celiac Sprue or dermatitis herpetiformis.
 XX
 PS Disclosure; Page 6; 115pp; English.
 XX
 CC The invention relates to a new HLA-binding peptide inhibitor, which is an
 CC analog of an immunogenic gluten oligopeptide of at least about 8 residues
 CC in length, altered by the replacement of one or more amino acids and that

best dates

CC binds tightly to HLA molecules, and is proteolytically stable and does
 CC not activate disease-specific T cells. Also disclosed is a computer for
 CC producing a three-dimensional representation of an HLA-DQ2 molecule bound
 CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
 CC comprises the sequence xPQPELPY. The HLA-binding peptide inhibitor is
 CC useful for preparing a composition for treating Celiac Sprue or
 CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
 CC predisposed to or have developed symptoms of type I diabetes. The current
 CC sequence represents an immunogenic gluten oligopeptide that may be
 CC modified to generate an HLA-binding peptide inhibitor.

SO Sequence 13 AA:

Query Match 100.0%; Score 42; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQPELPY 7
 |||||
 DB 6 PQPELPY 12

RESULT 29
 ADP91450
 ID ADP91450 standard; peptide; 13 AA.
 XX
 AC ADP91450;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Immunogenic gluten oligopeptide.
 XX
 KW Dermatological; antidiabetic; gene therapy; HLA; inhibitor; immunogenic;
 KW gluten; Celiac Sprue; dermatitis herpetiformis; HLA-DQ2 positive;
 KW type I diabetes; protein co-ordinate data.
 XX
 OS Synthetic.
 XX
 PN WO2003096984-A2.
 XX
 PD 27-NOV-2003.
 XX
 PE 14-MAY-2003; 2003WO-US015506.
 XX
 PR 14-MAY-2002; 2002US-0380761P.
 PR 28-JUN-2002; 2002US-0392782P.
 PR 31-OCT-2002; 2002US-0422933P.
 PR 20-NOV-2002; 2002US-0428033P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (SOLL) SOLID L M.
 PA (HANS) HANTSCH F.
 PA (SHAN) SHAN L.
 PA (KHOS) KHOSLA C.
 PA (QUAR) QUARSTEN H.
 XX
 PI Solid LM, Hausch F, Shan L, Khosla C, Quarsten H, Gray G;
 PI Kim C;
 XX
 DR WPI; 2004-053078/05.
 XX
 PT New HLA-binding peptide inhibitor that is an analog of an immunogenic
 PT given oligopeptide, useful for preparing a composition for treating
 PT e.g., Celiac Sprue or dermatitis herpetiformis.
 XX
 PS Claim 5, Page 112; 115pp; English.
 CC The invention relates to a new HLA-binding peptide inhibitor, which is an
 CC analog of an immunogenic gluten oligopeptide of at least about 8 residues
 CC in length, altered by the replacement of one or more amino acids and that
 CC binds tightly to HLA molecules, and is proteolytically stable and does
 CC not activate disease-specific T cells. Also disclosed is a computer for
 CC producing a three-dimensional representation of an HLA-DQ2 molecule bound

CC to an immunogenic gluten oligopeptide. The HLA-binding peptide inhibitor
 CC comprises the sequence xPQPELPY. The HLA-binding peptide inhibitor is
 CC useful for preparing a composition for treating Celiac Sprue or
 CC dermatitis herpetiformis, or HLA-DQ2 positive individuals who are either
 CC predisposed to or have developed symptoms of type I diabetes. The current
 CC sequence represents an immunogenic gluten oligopeptide that may be
 CC modified to generate an HLA-binding peptide inhibitor.

SO Sequence 13 AA:

Query Match 100.0%; Score 42; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PQPELPY 7
 |||||
 DB 1 PQPELPY 7

RESULT 30
 ADP91349
 ID ADP91349 standard; peptide; 13 AA.
 XX
 AC ADP91349;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE High affinity peptide substrate for tTGase.
 XX
 KW Dermatological; neuroprotective; cytostatic; vulnery; anticonvulsant;
 KW neurotropic; antiparkinsonian; tranquiliser; antiinflammatory;
 KW immunosuppressive; celiac sprue; dermatitis herpetiformis;
 KW tissue transglutaminase; tTGase; inhibitor; gluten;
 KW neurological disorder; cancer; wound healing; Huntington's disease;
 KW Alzheimer's disease; Parkinson's disease; food intolerance.
 XX
 OS Unidentified.
 XX
 PN WO2003096979-A2.
 XX
 PD 27-NOV-2003.
 XX
 PE 14-MAY-2003; 2003WO-US015343.
 XX
 PR 14-MAY-2002; 2002US-0380761P.
 PR 28-JUN-2002; 2002US-0392782P.
 PR 31-OCT-2002; 2002US-0422933P.
 PR 20-NOV-2002; 2002US-0428033P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 PA (KHOS) KHOSLA C, Hausch F, Parrot I, Shan L;
 PA (WPI) WPI; 2004-098857/10.
 XX
 PT Method useful for treatment of celiac sprue and/or dermatitis
 PT herpetiformis involves the use of tissue transglutaminase (tTGase)
 PT inhibitor to attenuate gluten toxicity.
 XX
 PS Disclosure; Page 9, 37pp; English.
 CC The invention relates to a method for the treatment of celiac sprue
 CC and/or dermatitis herpetiformis, involving the administration of tissue
 CC transglutaminase (tTGase) inhibitor to attenuate gluten toxicity in the
 CC patient. The method of the invention is useful for the treatment of a
 CC celiac sprue and dermatitis herpetiformis, or for the treatment of a
 CC disorder where tissue transglutaminase is a factor in disease etiology,
 CC such as a neurological disorder, cancer or wound healing. The method of
 CC the invention is also useful in the treatment of progressive supranuclear
 CC palsy, Huntington's, Alzheimer's and Parkinson's diseases, the aberrant
 CC activation of TGases may be caused by oxidative stress and inflammation.
 CC The formulation reduces the toxic effects of toxic gluten oligopeptides,
 CC thus attenuating or eliminates the damaging effects of gluten. The

CC formulation allows the celiac sprue individual to eat gluten-containing
 CC foodstuffs without ill effect, or at least to tolerate such foodstuffs in
 CC small or moderate quantities without inducing relapse. The current
 CC sequence represents a high affinity peptide substrate for tTase that
 CC acts as a glutenase resistant peptide. This peptide contains a glutamine
 CC formed by deamination.

XX Sequence 13 AA;

Query Match 100.0%; Score 42; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPHY 7
 1 POPELPHY 7

RESULT 31

ADH14656
 ID ADH14656 standard; peptide; 13 AA.

XX ADH14656;

XX 11-MAR-2004 (first entry)

XX Gliadin related epitope peptide.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX vaccine.

OS Synthetic.

PN WO2003104273-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.

XX (ISIS-) ISIS INNOVATION LTD.

XX Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

XX Example 6; Page 80; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 13 AA;

Query Match 100.0%; Score 42; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPHY 7
 7 POPELPHY 13

RESULT 32

AAU01828
 ID AAU01828 standard; peptide; 14 AA.

XX AAU01828;

XX 07-SEP-2001 (first entry)

XX Alpha-gliadin T-cell epitope described in coeliac disease #2.

XX Wheat; alpha-gliadin; T-cell epitope; coeliac disease;
 XX gluten intolerance; antagonist; transglutaminase; transgenic plant.

XX Triticum aestivum.

XX WO200125793-A2.

XX 12-APR-2001.

XX 02-OCT-2000; 2000WO-GB003760.

XX 01-OCT-1999; 99GB-00023306.

XX (ISIS-) ISIS INNOVATION LTD.

XX Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2001-300179/31.

XX Diagnosing coeliac disease or susceptibility to the disease in an
 PT individual, by detecting in vitro or in vivo T cells which bind
 PT immunodominant T cell epitope obtained from naturally occurring homolog
 PT of gliadin.

XX Example 6; Fig 12f; 107pp; English.

XX The sequence is a wheat alpha-gliadin T-cell epitope described in coeliac
 CC disease. The peptides of the invention are used to test mammalian
 CC (preferably human) susceptibility to coeliac disease (gluten and T cell
 CC intolerance). The peptides are contacted with a blood sample and T cell
 CC recognition measured, a positive T-cell recognition indicating a
 CC susceptibility to coeliac disease. The peptides are useful for inducing
 CC tolerance in an individual and antagonists to the peptides are useful for
 CC treating or preventing coeliac disease in an individual and for producing
 CC an antibody specific to them or a wild-type sequence. A mutant gliadin
 CC protein (or its fragment of 15 amino acids in length) whose wild-type
 CC sequence can be modified by transglutaminase to a sequence that comprises
 CC the epitope, but which has been modified in such a way that it does not
 CC contain sequence which can be modified by transglutaminase to a sequence
 CC that comprises the epitope is useful for decreasing the ability of gliadin
 CC protein to cause coeliac disease. Nucleic acids encoding proteins
 CC antagonistic to the T-cell binding of the epitopes are useful for
 CC obtaining a transgenic plant cell or seed and for the production of a
 CC protein. The resultant crop plant is useful for obtaining a product of a
 CC wheat plant, especially grain, which is optionally processed into flour
 CC or another grain product. Food comprising the antagonistic protein is
 CC useful instead of a wild-type gliadin

XX Sequence 14 AA;

Query Match 100.0%; Score 42; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPHY 7
 1 POPELPHY 7

corrected to match

PT Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX
PS Example 6; Page 80; 177pp; English.
XX
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 42; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PGPRLPY 7
DB 1 PGPRLPY 7
RESULT 36
ADH14560
ID ADH14560 standard; peptide; 14 AA.
XX
XX ADH14560;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Gliadin related epitope peptide.
DE
XX
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
XX Synthetic.
OS
XX WO2003104273-A2.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 05-JUN-2003; 2003WO-GB002450.
PE
XX
XX 05-JUN-2002; 2002GB-00012885.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX
XX Anderson RP, Hill AVS, Jewell DP;
PI
XX
XX WPI; 2004-043640/04.
DR
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX
PS Example 14; Page 66; 177pp; English.
XX
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 42; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

post duties

CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 42; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PGPRLPY 7
DB 1 PGPRLPY 7
RESULT 37
ADH14577
ID ADH14577 standard; peptide; 14 AA.
XX
XX ADH14577;
AC
XX
XX 11-MAR-2004 (first entry)
DT
XX
XX Gliadin related epitope peptide.
DE
XX
XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
XX Synthetic.
OS
XX WO2003104273-A2.
PN
XX
XX 18-DEC-2003.
PD
XX
XX 05-JUN-2003; 2003WO-GB002450.
PE
XX
XX 05-JUN-2002; 2002GB-00012885.
PR
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
XX
XX Anderson RP, Hill AVS, Jewell DP;
PI
XX
XX WPI; 2004-043640/04.
DR
XX
XX Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
XX
PS Example 14; Page 71; 177pp; English.
XX
XX The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 42; DB 8; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

post duties

QY 1 POPELPHY 7
 DB 1 POPELPHY 7

RESULT 38

ADH14574
 ID ADH14574 standard; peptide; 14 AA.

AC ADH14574;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PE 05-JUN-2003; 2003WO-GB002450.

PF 05-JUN-2002; 2002GB-00012865.

PS (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PS Example 14; Page 71; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

SQ Sequence 14 AA:

Query Match 100.0%; Score 42; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPHY 7
 DB 1 POPELPHY 7

RESULT 39

ADH16188
 ID ADH16188 standard; peptide; 14 AA.

AC ADH16188;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PE 05-JUN-2003; 2003WO-GB002450.

PS (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

DE Gliadin related epitope peptide.

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PE 05-JUN-2003; 2003WO-GB002450.

PF 05-JUN-2002; 2002GB-00012865.

PS (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

DR WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent

PT which are wheat gliadin T cell epitope capable of being recognized by T

PS Example 6; Fig 12f; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

SQ Sequence 14 AA:

Query Match 100.0%; Score 42; DB 8; Length 14;

Best Local Similarity 100.0%; Pred. No. 2.4;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPHY 7
 DB 1 POPELPHY 7

RESULT 40

ADH14659
 ID ADH14659 standard; peptide; 15 AA.

AC ADH14659;

DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.

KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PE 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Anderson RP, Hill AVS, Jewell DP;
 XX WPI; 2004-043640/04.
 XX
 XX Preventing or treating coeliac disease comprises administering agent
 XX PT which are wheat gliadin T cell epitope capable of being recognized by T
 XX PT cell receptor.
 XX
 XX Example 6; Page 80; 177pp; English.
 XX
 XX The present invention describes a method (M1) for preventing or treating
 XX CC coeliac disease. M1 comprises administering an agent (A) comprising a
 XX CC gliadin T cell epitope, which is capable of being recognised by a T cell
 XX CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 XX CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 XX CC be used in the preparation of a medicament for treating or preventing
 XX CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 XX CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 XX CC disease, in an individual, which involves determining whether T cells of
 XX CC the individual recognise the agent, recognition by the T cells indicating
 XX CC that the individual has, or is susceptible to, coeliac disease. The
 XX CC present sequence represents a peptide which is used in the
 XX CC exemplification of the present invention.

Query Match 100.0%; Score 42; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPY 7
 |||||
 4 POPELPY 10

RESULT 41
 ADH14658
 ID ADH14658 standard; peptide; 15 AA.
 XX
 XX ADH14658;
 XX
 XX 11-MAR-2004 (first entry)
 XX DT
 XX Gliadin related epitope peptide.
 XX DE
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX KM vaccine.
 XX OS
 XX Synthetic.
 XX OS
 XX WO2003104273-A2.
 XX FN
 XX 18-DEC-2003.
 XX PD
 XX 05-JUN-2003; 2003WO-GB002450.
 XX PF
 XX 05-JUN-2002; 2002GB-00012885.
 XX PR
 XX (ISIS-) ISIS INNOVATION LTD.
 XX PA
 XX Anderson RP, Hill AVS, Jewell DP;
 XX PI
 XX WPI; 2004-043640/04.
 XX DR
 XX Preventing or treating coeliac disease comprises administering agent
 XX PT which are wheat gliadin T cell epitope capable of being recognized by T
 XX PT cell receptor.
 XX PS
 XX Example 6; Page 80; 177pp; English.

first entry

XX The present invention describes a method (M1) for preventing or treating
 XX CC coeliac disease. M1 comprises administering an agent (A) comprising a
 XX CC gliadin T cell epitope, which is capable of being recognised by a T cell
 XX CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 XX CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 XX CC be used in the preparation of a medicament for treating or preventing
 XX CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 XX CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 XX CC disease, in an individual, which involves determining whether T cells of
 XX CC the individual recognise the agent, recognition by the T cells indicating
 XX CC that the individual has, or is susceptible to, coeliac disease. The
 XX CC present sequence represents a peptide which is used in the
 XX CC exemplification of the present invention.

Query Match 100.0%; Score 42; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELPY 7
 |||||
 4 POPELPY 10

RESULT 42
 AAU01804
 ID AAU01804 standard; protein; 17 AA.
 XX
 XX AAU01804;
 XX
 XX 07-SEP-2001 (first entry)
 XX DT
 XX Wheat A-gliadin 57-73, E57, 65, 72 mutant peptide.
 XX DE
 XX Wheat; A-gliadin; E57, 65, 72; coeliac disease; gluten intolerance;
 XX KM T-cell binding; antagonist; transglutaminase; transgenic plant; mutein.
 XX OS
 XX Triticum aestivum.
 XX OS
 XX WO200125793-A2.
 XX FN
 XX 12-APR-2001.
 XX PD
 XX 02-OCT-2000; 2000WO-GB003760.
 XX PF
 XX 01-OCT-1999; 99GB-00023306.
 XX PR
 XX (ISIS-) ISIS INNOVATION LTD.
 XX PA
 XX Anderson RP, Hill AVS, Jewell DP;
 XX PI
 XX WPI; 2001-300179/31.
 XX DR
 XX Diagnosing coeliac disease or susceptibility to the disease in an
 XX PT individual, by detecting in vitro or in vivo T cells which bind
 XX PT immunodominant T cell epitope obtained from naturally occurring homolog
 XX PT of gliadin.
 XX PS
 XX Disclosure; Page 4; 107pp; English.
 XX
 XX The sequence represents wheat A-gliadin T-cell epitope E57, 65, 72 which
 XX CC has Gln substituted with Glu at positions corresponding to 57, 65 and 72
 XX CC of the full length A-gliadin. The peptides of the invention are used to
 XX CC test mammalian (preferably human) susceptibility to coeliac disease
 XX CC (gluten intolerance). The peptides are contacted with a blood sample and
 XX CC T cell recognition measured, a positive T-cell recognition indicating a
 XX CC susceptibility to coeliac disease. The peptides are useful for inducing a
 XX CC tolerance in an individual and antagonists to the peptides are useful for
 XX CC treating or preventing coeliac disease in an individual and for producing
 XX CC an antibody specific to them or a wild-type sequence. A mutant gliadin
 XX CC protein (or its fragment of 15 amino acids in length) whose wild-type

converts to mutant

CC sequence can be modified by transglutaminase to a sequence that comprises
 CC the epitope, but which has been modified in such a way that it does not
 CC contain sequence which can be modified by transglutaminase to a sequence
 CC that comprises the epitope is useful for decreasing the ability of gliadin
 CC protein to cause Coeliac disease. Nucleic acids encoding proteins
 CC antagonistic to the T-cell binding of the epitopes are useful for
 CC obtaining a transgenic plant cell or seed and for the production of a
 CC protein. The resultant crop plant is useful for obtaining a product of a
 CC wheat plant, especially grain, which is optionally processed into flour
 CC or another grain product. Food comprising the antagonistic protein is
 CC useful instead of a wild-type gliadin

CC Sequence 17 AA;

Query Match 100.0%; Score 42; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 P0PELPY 7
 CC |||||
 CC 6 P0PELPY 12

RESULT 43
 AAU01843
 ID AAU01843 standard; peptide; 17 AA.
 AC AAU01843;
 DT 07-SRP-2001 (first entry)

CC Gliadin T-cell epitope described in coeliac disease.
 CC Wheat; gliadin; T-cell epitope; coeliac disease; gluten intolerance;
 CC antagonist; transglutaminase; transgenic plant.
 CC Triticum aestivum.
 CC MO200125793-A2.
 CC 12-APR-2001.
 CC 02-OCT-2000; 2000WO-GB003760.
 CC 01-OCT-1999; 99GB-00023306.
 CC (ISIS-) ISIS INNOVATION LTD.
 CC Anderson RP, Hill AVS, Jewell DP;
 CC WPI; 2001-300179/31.

CC Diagnosing coeliac disease or susceptibility to the disease in an
 CC individual, by detecting in vitro or in vivo T cells which bind
 CC immunodominant T cell epitope obtained from naturally occurring homolog
 CC of gliadin.

CC Example 6; Fig 12b; 107bp; English.

CC The sequence is a wheat gliadin T-cell epitope described in coeliac
 CC disease. The peptides of the invention are used to test mammalian
 CC (preferably human) susceptibility to coeliac disease (gluten
 CC intolerance). The peptides are contacted with a blood sample and T cell
 CC recognition measured, a positive T-cell recognition indicating a
 CC susceptibility to coeliac disease. The peptides are useful for inducing
 CC tolerance in an individual and antagonists to the peptides are useful for
 CC treating or preventing coeliac disease in an individual and for producing
 CC an antibody specific to them or a wild-type sequence. A mutant gliadin
 CC protein for its fragment of 15 amino acids in length whose wild-type
 CC sequence can be modified by transglutaminase to a sequence that comprises
 CC the epitope, but which has been modified in such a way that it does not
 CC contain sequence which can be modified by transglutaminase to a sequence
 CC that comprises the epitope is useful for decreasing the ability of gliadin

CC protein to cause Coeliac disease. Nucleic acids encoding proteins
 CC antagonistic to the T-cell binding of the epitopes are useful for
 CC obtaining a transgenic plant cell or seed and for the production of a
 CC protein. The resultant crop plant is useful for obtaining a product of a
 CC wheat plant, especially grain, which is optionally processed into flour
 CC or another grain product. Food comprising the antagonistic protein is
 CC useful instead of a wild-type gliadin

CC Sequence 17 AA;

Query Match 100.0%; Score 42; DB 4; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 P0PELPY 7
 CC |||||
 CC 6 P0PELPY 12

RESULT 44
 AAU01843
 ID AAU01843 standard; peptide; 17 AA.
 AC AAU01843;
 DT 07-SRP-2001 (first entry)

CC Wheat peptide antagonist for A-gliadin 57-73 Q665 #5.
 CC Wheat; A-gliadin; 57-75 Q665; coeliac disease; gluten intolerance;
 CC T-cell binding; antagonist; transglutaminase; transgenic plant.
 CC Triticum aestivum.
 CC MO200125793-A2.
 CC 12-APR-2001.
 CC 02-OCT-2000; 2000WO-GB003760.
 CC 01-OCT-1999; 99GB-00023306.
 CC (ISIS-) ISIS INNOVATION LTD.
 CC Anderson RP, Hill AVS, Jewell DP;
 CC WPI; 2001-300179/31.

CC Diagnosing coeliac disease or susceptibility to the disease in an
 CC individual, by detecting in vitro or in vivo T cells which bind
 CC immunodominant T cell epitope obtained from naturally occurring homolog
 CC of gliadin.

CC Example 11; Page 58; 107bp; English.

CC The sequence represents a gliadin peptide corresponding to A-gliadin 57-
 CC 73 which is naturally polymorphic in that region and is antagonistic to A
 CC -gliadin 57-73 Q665 interferon gamma ELISPOT (not defined) response. The
 CC peptides of the invention are used to test mammalian (preferably human)
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are
 CC contacted with a blood sample and T cell recognition measured, a positive
 CC T-cell recognition indicating a susceptibility to coeliac disease. The
 CC peptides are useful for inducing tolerance in an individual and
 CC antagonists to the peptides are useful for treating or preventing coeliac
 CC disease in an individual and for producing an antibody specific to them
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
 CC amino acids in length) whose wild-type sequence can be modified by
 CC transglutaminase to a sequence that comprises the epitope, but which has
 CC been modified in such a way that it does not contain sequence which can
 CC be modified by transglutaminase to a sequence that comprises the epitope
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
 CC binding of the epitopes are useful for obtaining a transgenic plant cell

OY 1 POPELPY 7
 |||||
 Db 6 POPELPY 12

RESULT 46

AAU01803 standard; protein; 17 AA.

AAU01803;

07-SEP-2001 (first entry)

Wheat A-gliadin 57-73, E65, 72 mutant peptide.

Wheat; A-gliadin; E65, 72; coeliac disease; gluten intolerance; gluten intolerance; antagonist; transglutaminase; transgenic plant; mutein.

Triticum aestivum.

MO200125793-A2.

12-APR-2001.

02-OCT-2000; 2000MO-SB003760.

01-OCT-1999; 99GB-00023306.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2001-300179/31.

Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.

Disclosure; Page 4; 107pp; English.

The sequence represents wheat A-gliadin T-cell epitope E65, 72, which has full length A-gliadin. The peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can be modified by transglutaminase to a sequence that comprises the epitope is useful for decreasing the ability of gliadin protein to cause Coeliac disease. Nucleic acids encoding proteins antagonistic to the T-cell binding of the epitopes are useful for obtaining a transgenic plant cell or seed and for the production of a protein. The resultant crop plant is useful for obtaining a product of a wheat plant, especially grain, which is optionally processed into flour or another grain product. Food comprising the antagonistic protein is useful instead of a wild-type gliadin

Sequence 17 AA;

Query Match 100.0%; Score 42; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;

1 POPELPY 7
 |||||
 Db 6 POPELPY 12

RESULT 47

AAU01802 standard; protein; 17 AA.

AAU01802;

07-SEP-2001 (first entry)

Wheat A-gliadin 57-73, E57, 65 mutant peptide.

Wheat; A-gliadin; E57, 65; coeliac disease; gluten intolerance; gluten intolerance; antagonist; transglutaminase; transgenic plant; mutein.

Triticum aestivum.

MO200125793-A2.

12-APR-2001.

02-OCT-2000; 2000MO-SB003760.

01-OCT-1999; 99GB-00023306.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2001-300179/31.

Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.

Disclosure; Page 4; 107pp; English.

The sequence represents wheat A-gliadin T-cell epitope E57, 65, which has full length A-gliadin. The peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can be modified by transglutaminase to a sequence that comprises the epitope is useful for decreasing the ability of gliadin protein to cause Coeliac disease. Nucleic acids encoding proteins antagonistic to the T-cell binding of the epitopes are useful for obtaining a transgenic plant cell or seed and for the production of a protein. The resultant crop plant is useful for obtaining a product of a wheat plant, especially grain, which is optionally processed into flour or another grain product. Food comprising the antagonistic protein is useful instead of a wild-type gliadin

Sequence 17 AA;

Query Match 100.0%; Score 42; DB 4; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.9; Mismatches 0; Indels 0; Gaps 0;

1 POPELPY 7
 |||||
 Db 6 POPELPY 12

RESULT 48

ADH14516
ID ADH14516 standard; peptide; 17 AA.
XX
AC ADH14516;
XX
DT 11-MAR-2004 (first entry)
XX
DE Gliadin related epitope peptide SEQ ID NO:6.
XX
KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
OS Synthetic.
XX
PN WO2003104273-A2.
XX
PD 18-DEC-2003.
XX
PF 05-JUN-2003; 2003WO-GB002450.
XX
PR 05-JUN-2002; 2002GB-00012885.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2004-043640/04.
XX
PT Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
PS Example 1; SEQ ID NO 6; 177pp; English.
XX
CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
CC
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 42; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 POPELPPY 7
DB 6 POPELPPY 12
XX
RESULT 49
ADH14564
ID ADH14564 standard; peptide; 17 AA.
XX
AC ADH14564;
XX
DT 11-MAR-2004 (first entry)
XX
DE Gliadin related epitope peptide.
XX
KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
OS Synthetic.

XX
PN WO2003104273-A2.
XX
PD 18-DEC-2003.
XX
PF 05-JUN-2003; 2003WO-GB002450.
XX
PR 05-JUN-2002; 2002GB-00012885.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX
DR WPI; 2004-043640/04.
XX
PT Preventing or treating coeliac disease comprises administering agent
PT which are wheat gliadin T cell epitope capable of being recognized by T
PT cell receptor.
XX
PS Example 14; Page 69; 177pp; English.
XX
CC The present invention describes a method (M1) for preventing or treating
CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a peptide which is used in the
CC exemplification of the present invention.
CC
SQ Sequence 17 AA;
XX
Query Match 100.0%; Score 42; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 POPELPPY 7
DB 6 POPELPPY 12
XX
RESULT 50
ADH14512
ID ADH14512 standard; peptide; 17 AA.
XX
AC ADH14512;
XX
DT 11-MAR-2004 (first entry)
XX
DE Gliadin related epitope peptide SEQ ID NO:2.
XX
KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
KM vaccine.
XX
OS Synthetic.
XX
PN WO2003104273-A2.
XX
PD 18-DEC-2003.
XX
PF 05-JUN-2003; 2003WO-GB002450.
XX
PR 05-JUN-2002; 2002GB-00012885.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX
PI Anderson RP, Hill AVS, Jewell DP;
XX

DR MPI, 2004-043640/04.

Preventing or treating coeliac disease comprises administering agent which are wheat gliadin T cell epitope capable of being recognized by T cell receptor.

Claim 1; SEQ ID NO 2; 177pp; English.

The present invention describes a method (M1) for preventing or treating coeliac disease. M1 comprises administering an agent (A) comprising a gliadin T cell epitope, which is capable of being recognised by a T cell receptor, to an individual. Gliadin is a component of gluten. (A) has gastrointestinal activity, and can be used in vaccines. The agent (A) can be used in the preparation of a medicament for treating or preventing coeliac disease. (A) can also be used in the preparation of a diagnostic means for use in diagnosing coeliac disease, or susceptibility to coeliac disease, in an individual, which involves determining whether T cells of the individual recognise the agent, recognition by the T cells indicating that the individual has, or is susceptible to, coeliac disease. The present sequence represents a peptide which is used in the exemplification of the present invention.

Sequence 17 AA:

Query Match	100.0%	Score 42;	DB 8;	Length 17;
Best Local Similarity	100.0%	Pred. No. 2.9;		
Matches	7;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;
1 POPELPY 7				
6 POPELPY 12				

RESULT 51

ADH14635

ADH14635 standard; peptide; 17 AA.

ADH14635;

11-MAR-2004 (first entry)

Gliadin related epitope peptide.

coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal; vaccine.

Synthetic.

WO2003104273-A2.

18-DEC-2003.

05-JUN-2003; 2003WO-GB002450.

05-JUN-2002; 2002GB-00012885.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2004-043640/04.

Preventing or treating coeliac disease comprises administering agent which are wheat gliadin T cell epitope capable of being recognized by T cell receptor.

Example 2; Page 79; 177pp; English.

The present invention describes a method (M1) for preventing or treating coeliac disease. M1 comprises administering an agent (A) comprising a gliadin T cell epitope, which is capable of being recognised by a T cell receptor, to an individual. Gliadin is a component of gluten. (A) has gastrointestinal activity, and can be used in vaccines. The agent (A) can

CC	be used in the preparation of a medicament for treating or preventing
CC	coeliac disease. (A) can also be used in the preparation of a diagnostic
CC	means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC	disease, in an individual, which involves determining whether T cells of
CC	the individual recognise the agent, recognition by the T cells indicating
CC	that the individual has, or is susceptible to, coeliac disease. The
CC	present sequence represents a peptide which is used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 17 AA;
Query Match	100.0%; Score 42; DB 8; Length 17;
Best Local Similarity	100.0%; Pred. No. 2.9;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 POPELPY 7 6 POPELPY 12
Db	
RESULT 52	
ID	ADH16210 standard; peptide; 17 AA.
AC	ADH16210;
XX	
D7	11-MAR-2004 (first entry)
XX	
DE	Gliadin related epitope peptide.
XX	
KM	coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal; vaccine.
XX	
OS	Synthetic.
XX	
PN	WO2003104273-A2.
PD	
16-DEC-2003.	
PF	05-JUN-2003; 2003WO-GB002450.
XX	
PR	05-JUN-2002; 2002GB-00012885.
XX	
PA	(ISIS-) ISIS INNOVATION LTD.
F1	Andersen RP, Hill AVS, Jewell DP;
DR	
WPI; 2004-043640/04.	
P7	Preventing or treating coeliac disease comprises administering agent
P7	which are wheat gliadin T cell epitope capable of being recognized by T
F1	cell receptor.
XX	
XX	
XX	
Example 10; Fig 17; 177pp; English.	
XX	
CC	The present invention describes a method (M1) for preventing or treating
CC	coeliac disease. M1 comprises administering an agent (A) comprising a
CC	gliadin T cell epitope, which is capable of being recognised by a T cell
CC	receptor, to an individual. Gliadin is a component of gluten. (A) has
CC	gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC	be used in the preparation of a medicament for treating or preventing
CC	coeliac disease. (A) can also be used in the preparation of a diagnostic
CC	means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC	disease, in an individual, which involves determining whether T cells of
CC	the individual recognise the agent, recognition by the T cells indicating
CC	that the individual has, or is susceptible to, coeliac disease. The
CC	present sequence represents a peptide which is used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 17 AA;
Query Match	100.0%; Score 42; DB 8; Length 17;
Best Local Similarity	100.0%; Pred. NO. 2.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
| | | | |
| | | | |
Db 6 POPELPY 12

RESULT 53

ADH14518
ID ADH14518 standard; peptide; 17 AA.

XX ADH14518;

XX 11-MAR-2004 (first entry)

XX Gliadin related epitope peptide SEQ ID NO:8.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

XX vaccine.

XX Synthetic.

XX WO2003104273-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.

XX (ISIS-) ISIS INNOVATION LTD.

XX Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent

XX PT which are wheat gliadin T cell epitope capable of being recognized by T

XX cell receptor.

XX Example 1; SEQ ID NO 8; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
XX coeliac disease. M1 comprises administering an agent (A) comprising a
XX gliadin T cell epitope, which is capable of being recognised by a T cell
XX receptor, to an individual. Gliadin is a component of gluten. (A) has
XX been used in the preparation of a medicament for treating or preventing
XX coeliac disease. (A) can also be used in the preparation of a diagnostic
XX means for use in diagnosing coeliac disease, or susceptibility to coeliac
XX disease, in an individual, which involves determining whether T cells of
XX the individual recognise the agent, recognition by the T cells indicating
XX that the individual has, or is susceptible to, coeliac disease. The
XX present sequence represents a peptide which is used in the
XX exemplification of the present invention.

XX Sequence 17 AA;

QY Query Match 100.0%; Score 42; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
| | | | |
| | | | |
Db 6 POPELPY 12

RESULT 54

ADH16182
ID ADH16182 standard; peptide; 17 AA.

XX ADH16182;

DT 11-MAR-2004 (first entry)

XX Gliadin related epitope peptide.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

XX vaccine.

XX Synthetic.

XX WO2003104273-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.

XX (ISIS-) ISIS INNOVATION LTD.

XX Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent

XX PT which are wheat gliadin T cell epitope capable of being recognized by T

XX cell receptor.

XX Example 6; Fig 12a; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
XX coeliac disease. M1 comprises administering an agent (A) comprising a
XX gliadin T cell epitope, which is capable of being recognised by a T cell
XX receptor, to an individual. Gliadin is a component of gluten. (A) has
XX been used in the preparation of a medicament for treating or preventing
XX coeliac disease. (A) can also be used in the preparation of a diagnostic
XX means for use in diagnosing coeliac disease, or susceptibility to coeliac
XX disease, in an individual, which involves determining whether T cells of
XX the individual recognise the agent, recognition by the T cells indicating
XX that the individual has, or is susceptible to, coeliac disease. The
XX present sequence represents a peptide which is used in the
XX exemplification of the present invention.

XX Sequence 17 AA;

QY Query Match 100.0%; Score 42; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
| | | | |
| | | | |
Db 6 POPELPY 12

RESULT 55

ADH14557
ID ADH14557 standard; peptide; 17 AA.

XX ADH14557;

XX 11-MAR-2004 (first entry)

XX Gliadin related epitope peptide.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

XX vaccine.

XX Synthetic.

XX WO2003104273-A2.

XX 18-DEC-2003.

BF 05-JUN-2003; 2003WO-GB002450.
 XX
 XX 05-JUN-2002; 2002GB-00012885.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 XX
 XX Anderson RP, Hill AVS, Jewell DP;
 XX
 XX WPI; 2004-043640/04.
 XX
 XX Preventing or treating coeliac disease comprises administering agent
 XX which are wheat gliadin T cell epitope capable of being recognized by T
 XX cell receptor.
 XX
 XX Example 14; Page 65; 177pp; English.
 XX
 XX The present invention describes a method (M1) for preventing or treating
 XX coeliac disease. M1 comprises administering an agent (A) comprising a
 XX gliadin T cell epitope, which is capable of being recognised by a T cell
 XX receptor, to an individual. Gliadin is a component of gluten. (A) has
 XX gastrointestinal activity, and can be used in vaccines. The agent (A) can
 XX be used in the preparation of a medicament for treating or preventing
 XX coeliac disease. (A) can also be used in the preparation of a diagnostic
 XX means for use in diagnosing coeliac disease, or susceptibility to coeliac
 XX disease, in an individual, which involves determining whether T cells of
 XX the individual recognise the agent, recognition by the T cells indicating
 XX that the individual has, or is susceptible to, coeliac disease. The
 XX present sequence represents a peptide which is used in the
 XX exemplification of the present invention.
 XX
 XX Sequence 17 AA;
 XX
 XX Query Match 100.0%; Score 42; DB 8; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 2.9; 0; Indels 0; Gaps 0;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 POPELPY 7
 XX |||||
 XX 6 POPELPY 12
 XX
 XX
 XX RESULT 56
 XX ADH14653
 XX ADH14653 standard; peptide; 17 AA.
 XX
 XX AC ADH14653;
 XX
 XX DT 11-MAR-2004 (first entry)
 XX
 XX 05 Gliadin related epitope peptide.
 XX
 XX 05 coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX vaccine.
 XX
 XX 05 Synthetic.
 XX
 XX 05 WO2003104273-A2.
 XX
 XX 05 18-DEC-2003.
 XX
 XX 05 05-JUN-2003; 2003WO-GB002450.
 XX
 XX 05 05-JUN-2002; 2002GB-00012885.
 XX
 XX 05 (ISIS-) ISIS INNOVATION LTD.
 XX
 XX 05 Anderson RP, Hill AVS, Jewell DP;
 XX
 XX 05 WPI; 2004-043640/04.
 XX
 XX Preventing or treating coeliac disease comprises administering agent
 XX which are wheat gliadin T cell epitope capable of being recognized by T
 XX cell receptor.

XX
 XX Example 6; Page 80; 177pp; English.
 XX
 XX The present invention describes a method (M1) for preventing or treating
 XX coeliac disease. M1 comprises administering an agent (A) comprising a
 XX gliadin T cell epitope, which is capable of being recognised by a T cell
 XX receptor, to an individual. Gliadin is a component of gluten. (A) has
 XX gastrointestinal activity, and can be used in vaccines. The agent (A) can
 XX be used in the preparation of a medicament for treating or preventing
 XX coeliac disease. (A) can also be used in the preparation of a diagnostic
 XX means for use in diagnosing coeliac disease, or susceptibility to coeliac
 XX disease, in an individual, which involves determining whether T cells of
 XX the individual recognise the agent, recognition by the T cells indicating
 XX that the individual has, or is susceptible to, coeliac disease. The
 XX present sequence represents a peptide which is used in the
 XX exemplification of the present invention.
 XX
 XX Sequence 17 AA;
 XX
 XX Query Match 100.0%; Score 42; DB 8; Length 17;
 XX Best Local Similarity 100.0%; Pred. No. 2.9; 0; Indels 0; Gaps 0;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 POPELPY 7
 XX |||||
 XX 6 POPELPY 12
 XX
 XX
 XX RESULT 57
 XX ADH16183
 XX ADH16183 standard; peptide; 17 AA.
 XX
 XX AC ADH16183;
 XX
 XX DT 11-MAR-2004 (first entry)
 XX
 XX 05 Gliadin related epitope peptide.
 XX
 XX 05 coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX vaccine.
 XX
 XX 05 Synthetic.
 XX
 XX 05 WO2003104273-A2.
 XX
 XX 05 18-DEC-2003.
 XX
 XX 05 05-JUN-2003; 2003WO-GB002450.
 XX
 XX 05 05-JUN-2002; 2002GB-00012885.
 XX
 XX 05 (ISIS-) ISIS INNOVATION LTD.
 XX
 XX 05 Anderson RP, Hill AVS, Jewell DP;
 XX
 XX 05 WPI; 2004-043640/04.
 XX
 XX Preventing or treating coeliac disease comprises administering agent
 XX which are wheat gliadin T cell epitope capable of being recognized by T
 XX cell receptor.
 XX
 XX Example 6; Fig 12b; 177pp; English.
 XX
 XX The present invention describes a method (M1) for preventing or treating
 XX coeliac disease. M1 comprises administering an agent (A) comprising a
 XX gliadin T cell epitope, which is capable of being recognised by a T cell
 XX receptor, to an individual. Gliadin is a component of gluten. (A) has
 XX gastrointestinal activity, and can be used in vaccines. The agent (A) can
 XX be used in the preparation of a medicament for treating or preventing
 XX coeliac disease. (A) can also be used in the preparation of a diagnostic
 XX means for use in diagnosing coeliac disease, or susceptibility to coeliac
 XX disease, in an individual, which involves determining whether T cells of
 XX the individual recognise the agent, recognition by the T cells indicating

CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

CC Sequence 17 AA;

Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPELPY 7
 |||||
 DB 6 PPELPY 12

RESULT 58
 ADH14517
 ID ADH14517 standard; peptide; 17 AA.

AC ADH14517;
 DT 11-MAR-2004 (first entry)
 XX Gliadin related epitope peptide SEQ ID NO:7.

DE coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

PS Example 1; SEQ ID NO 7; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastroenteric activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPELPY 7
 |||||
 DB 6 PPELPY 12

RESULT 59
 ADH14633
 ID ADH14633 standard; peptide; 17 AA.

AC ADH14633;
 DT 11-MAR-2004 (first entry)
 XX Gliadin related epitope peptide.

DE coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX vaccine.

OS Synthetic.

PN WO2003104273-A2.

PD 18-DEC-2003.

PF 05-JUN-2003; 2003WO-GB002450.

PR 05-JUN-2002; 2002GB-00012885.

PA (ISIS-) ISIS INNOVATION LTD.

PI Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

PS Example 15; Page 75; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastroenteric activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PPELPY 7
 |||||
 DB 6 PPELPY 12

RESULT 60
 ADH14693
 ID ADH14693 standard; peptide; 17 AA.

AC ADH14693;
 DT 11-MAR-2004 (first entry)

DE Gliadin related epitope peptide.
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

KW vaccine.
 XX
 OS Synthetic.
 XX
 PN MO2003104273-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 05-JUN-2003; 2003WO-GB002450.
 XX
 PR 05-JUN-2002; 2002GB-00012885.
 XX
 RA (ISIS-) ISIS INNOVATION LTD.
 XX
 RI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI; 2004-043640/04.
 XX
 PE Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 cell receptor.
 XX
 PS Example 11; Page 84; 177pp; English.
 XX
 SC The present invention describes a method (M1) for preventing or treating
 coeliac disease. M1 comprises administering an agent (A) comprising a
 gliadin T cell epitope, which is capable of being recognised by a T cell
 receptor, to an individual. Gliadin is a component of gluten. (A) has
 gastrointestinal activity, and can be used in vaccines. The agent (A) can
 be used in the preparation of a medicament for treating or preventing
 coeliac disease. (A) can also be used in the preparation of a diagnostic
 means for use in diagnosing coeliac disease, or susceptibility to coeliac
 disease, in an individual, which involves determining whether T cells of
 the individual recognise the agent, recognition by the T cells indicating
 that the individual has, or is susceptible to, coeliac disease. The
 present sequence represents a peptide which is used in the
 exemplification of the present invention.
 XX
 SO Sequence 17 AA;
 XX
 Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 POPELPY 7
 |||||
 Db 6 POPELPY 12
 XX
 RESULT 61
 ADH14539
 ID ADH14539 standard; peptide; 17 AA.
 XX
 AC ADH14539;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Control peptide SEQ ID NO:29.
 XX
 KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 vaccine.
 XX
 OS Synthetic.
 XX
 PN MO2003104273-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 05-JUN-2003; 2003WO-GB002450.
 XX
 PR 05-JUN-2002; 2002GB-00012885.
 XX
 RA (ISIS-) ISIS INNOVATION LTD.
 XX
 RI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI; 2004-043640/04.
 XX
 PE Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 cell receptor.
 XX
 PS Example 14; Page 86; 177pp; English.
 XX
 SC The present invention describes a method (M1) for preventing or treating
 coeliac disease. M1 comprises administering an agent (A) comprising a

XX
 PI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI; 2004-043640/04.
 XX
 PE Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 cell receptor.
 XX
 PS Example 13; SEQ ID NO 29; 177pp; English.
 XX
 SC The present invention describes a method (M1) for preventing or treating
 coeliac disease. M1 comprises administering an agent (A) comprising a
 gliadin T cell epitope, which is capable of being recognised by a T cell
 receptor, to an individual. Gliadin is a component of gluten. (A) has
 gastrointestinal activity, and can be used in vaccines. The agent (A) can
 be used in the preparation of a medicament for treating or preventing
 coeliac disease. (A) can also be used in the preparation of a diagnostic
 means for use in diagnosing coeliac disease, or susceptibility to coeliac
 disease, in an individual, which involves determining whether T cells of
 the individual recognise the agent, recognition by the T cells indicating
 that the individual has, or is susceptible to, coeliac disease. The
 present sequence represents a peptide which is used in the
 exemplification of the present invention.
 XX
 SO Sequence 17 AA;
 XX
 Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 OY 1 POPELPY 7
 |||||
 Db 6 POPELPY 12
 XX
 RESULT 62
 ADH14558
 ID ADH14558 standard; peptide; 17 AA.
 XX
 AC ADH14558;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Gliadin related epitope peptide.
 XX
 KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 vaccine.
 XX
 OS Synthetic.
 XX
 PN MO2003104273-A2.
 XX
 PD 18-DEC-2003.
 XX
 PF 05-JUN-2003; 2003WO-GB002450.
 XX
 PR 05-JUN-2002; 2002GB-00012885.
 XX
 RA (ISIS-) ISIS INNOVATION LTD.
 XX
 RI Anderson RP, Hill AVS, Jewell DP;
 XX
 DR WPI; 2004-043640/04.
 XX
 PE Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 cell receptor.
 XX
 PS Example 14; Page 66; 177pp; English.
 XX
 SC The present invention describes a method (M1) for preventing or treating
 coeliac disease. M1 comprises administering an agent (A) comprising a

CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
 DB 6 POPELPY 12

RESULT 63
 ADH14537
 ID ADH14537 standard; peptide; 17 AA.
 AC ADH14537;
 XX 11-MAR-2004 (first entry)
 DT
 DE Control peptide SEQ ID NO:27.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KM vaccine.

XX Synthetic.

XX WO2003104273-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.

XX (ISIS-) ISIS INNOVATION LTD.

XX Anderson RP, Hill AVS, Jewell DP,

XX WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

PS Example 13; SEQ ID NO 27; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 17 AA;

RESULT 64
 ADH14575
 ID ADH14575 standard; peptide; 17 AA.
 AC ADH14575;
 XX 11-MAR-2004 (first entry)
 DT
 DE Gliadin related epitope peptide.
 XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 KM vaccine.
 XX Synthetic.
 XX WO2003104273-A2.
 XX 18-DEC-2003.
 XX 05-JUN-2003; 2003WO-GB002450.
 XX 05-JUN-2002; 2002GB-00012885.
 XX (ISIS-) ISIS INNOVATION LTD.
 XX Anderson RP, Hill AVS, Jewell DP,
 XX WPI; 2004-043640/04.

PT Preventing or treating coeliac disease comprises administering agent
 PT which are wheat gliadin T cell epitope capable of being recognized by T
 PT cell receptor.

PS Example 14; Page 71; 177pp; English.

CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 42; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 7
 DB 6 POPELPY 12

RESULT 65
 AAU01807
 ID AAU01807 standard; peptide; 20 AA.

XX AC AAU01807;
 XX DT 07-SEP-2001 (first entry)
 XX DE Wheat A-gliadin 56-75 transglutaminase treated peptide.
 XX KW Wheat; A-gliadin; 56-75 peptide; coeliac disease; gluten intolerance;
 XX KW T-cell binding; antagonist; transglutaminase; transgenic plant.
 XX OS Triticum aestivum.
 XX PN WO200125793-A2.
 XX PD 12-APR-2001.
 XX PF 02-OCT-2000; 2000WO-GB003760.
 XX PR 01-OCT-1999; 99GB-00023306.
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX PI Anderson RP, Hill AVS, Jewell DP;
 XX DR WFI; 2001-300179/31.
 XX PT Diagnosing coeliac disease or susceptibility to the disease in an
 XX PT individual, by detecting in vitro or in vivo T cells which bind
 XX PT immunodominant T cell epitope obtained from naturally occurring homolog
 XX PT of gliadin.
 XX PS Example 3; Page 40; 107pp; English.
 CC The sequence represents wheat A-gliadin 56-75 peptide, which has been
 CC treated with transglutaminase resulting in the Glu at position
 CC corresponding to 65 in the full length A-gliadin being converted Glu. The
 CC peptides of the invention are used to test mammalian (preferably human)
 CC susceptibility to coeliac disease (gluten intolerance). The peptides are
 CC contacted with a blood sample and T cell recognition measured, a positive
 CC T-cell recognition indicating a susceptibility to coeliac disease. The
 CC peptides are useful for inducing tolerance in an individual and
 CC antagonists to the peptides are useful for treating or preventing coeliac
 CC disease in an individual and for producing an antibody specific to them
 CC or a wild-type sequence. A mutant gliadin protein (or its fragment of 15
 CC amino acids in length) whose wild-type sequence can be modified by
 CC transglutaminase to a sequence that comprises the epitope, but which has
 CC been modified in such a way that it does not contain sequence which can
 CC be modified by transglutaminase to a sequence that comprise the epitope
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
 CC binding of the epitopes are useful for obtaining a transgenic plant cell
 CC or seed and for the production of a protein. The resultant crop plant is
 CC useful for obtaining a product of a wheat plant, especially grain, which
 CC is optionally processed into flour or another grain product. Food
 CC comprising the antagonistic protein is useful instead of a wild-type
 CC gliadin
 XX SC Sequence 20 AA;
 XX
 XX Query Match 100.0%; Score 42; DB 4; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 3.4; Indels 0; Gaps 0;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 POPELPY 7
 XX |||||
 XX DB 7 POPELPY 13
 XX
 XX RESULT 66
 XX ADH14521
 XX ADH14521 standard; peptide; 20 AA.
 XX AC ADH14521;

converted to matches

XX DT 11-MAR-2004 (first entry)
 XX DE Gliadin related epitope peptide SEQ ID NO:11.
 XX KW coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;
 XX KW vaccine.
 XX OS Synthetic.
 XX PN NO2003104273-A2.
 XX PD 18-DEC-2003.
 XX PF 05-JUN-2003; 2003WO-GB002450.
 XX PR 05-JUN-2002; 2002GB-00012895.
 XX PA (ISIS-) ISIS INNOVATION LTD.
 XX PI Anderson RP, Hill AVS, Jewell DP;
 XX DR WFI; 2004-043640/04.
 XX PT Preventing or treating coeliac disease comprises administering agent
 XX PT which are wheat gliadin T cell epitope capable of being recognized by T
 XX PT cell receptor.
 XX PS Example 4; SEQ ID NO 11; 177pp; English.
 CC The present invention describes a method (M1) for preventing or treating
 CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor, to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a peptide which is used in the
 CC exemplification of the present invention.
 XX SC Sequence 20 AA;
 XX
 XX Query Match 100.0%; Score 42; DB 8; Length 20;
 XX Best Local Similarity 100.0%; Pred. No. 3.4; Indels 0; Gaps 0;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 POPELPY 7
 XX |||||
 XX DB 7 POPELPY 13
 XX
 XX RESULT 67
 XX ADF91350
 XX ADF91350 standard; peptide; 33 AA.
 XX AC ADF91350;
 XX DT 26-FEB-2004 (first entry)
 XX DE High affinity peptide substrate for tTGase.
 XX KW dermatological; neuroprotective; cytosolic; vulnary; anticonvulsant;
 XX KW neurotropic; antiparkinsonian; tranquiliser; antiinflammatory;
 XX KW immunosuppressive; coeliac sprue; dermatitis herpetiformis;
 XX KW tissue transglutaminase; tTGase; inhibitor; gluten;
 XX KW neurological disorder; cancer; wound healing; Huntington's disease;
 XX KW Alzheimer's disease; Parkinson's disease; food intolerance.
 XX OS Unidentified.

part of data

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post sales

XX WO2003096979-A2.
PN

PD 27-NOV-2003

PF 14-MAY-2003; 2003WO-US015343.

PR 14-MAY-2002; 2002US-0380761P.

PR 31-OCT-2002; 2002US-0422933P.

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XX 35

herpetiformis involves the use

[illegible][illegible]

and/or dermatitis herpetiformis

CC patient. The method of the in-

disorder where tissue transglutaminase

CC such as a neurological disorder
CC the invention is also useful

activation of TGases may be a
palsy, Huntington's, Alzheimer's

CC thus attenuating or eliminating

CC formulation allows the cellular
CC feedstocks without ill effect

small or moderate quantities
experience represents a high at

acts as a glutenase resistant form of protein

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Best Local Similarity	100.0%;
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Search completed: December 15, 2011

Search completed: December 15, 2004, 15:37:07
Job time : 153 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07, Search time 13.7083 Seconds

(Without alignments)
49.132 Million cell updates/sec

Title: US-10-089-700-1

Sequence: 1 P0PELPY 7

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 263416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 263416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	39	92.9	286	1 EEWTA	alpha/beta-gliadin
2	39	92.9	286	2 S07923	alpha/beta-gliadin
3	39	92.9	291	2 T06498	alpha/beta-gliadin
4	39	92.9	297	2 T06500	alpha/beta-gliadin
5	39	92.9	307	2 S10015	alpha/beta-gliadin
6	39	92.9	326	2 D23364	alpha/beta-gliadin
7	37	88.1	541	1 S45428	PFT12 protein - y
8	36	85.7	165	2 E86537	hypothetical prote
9	36	85.7	165	2 D72085	hypothetical prote
10	36	85.7	208	2 S36155	paired box protein
11	36	85.7	342	2 S57652	transcription fact
12	36	85.7	361	2 A40023	paired box homolog
13	35	83.3	289	2 T52354	hypothetical prote
14	35	83.3	306	2 G96014	hypothetical prote
15	35	83.3	332	2 T20107	hypothetical prote
16	35	83.3	437	2 T00127	hypothetical prote
17	35	83.3	461	2 J04972	steroidogenic fact
18	35	83.3	666	2 S75289	ribonuclease II -
19	35	83.3	686	2 AB2362	ribonuclease II (i
20	35	83.3	769	2 S55554	male-specific leth
21	35	83.3	781	2 T26080	hypothetical prote
22	35	83.3	787	2 S09411	DNA translocase sp
23	35	83.3	788	2 G89901	hypothetical prote
24	34	81.0	213	1 D70416	phosphoglycolate p
25	34	81.0	254	2 A87582	conjugal transfer
26	34	81.0	348	2 T04184	hypothetical prote
27	34	81.0	926	2 AG1860	hypothetical prote
28	33	78.6	162	2 A48464	filarial antigen S
29	33	78.6	261	2 AB2966	conserved hypothet

30	33	78.6	261	2 B98317	ATP synthase chain
31	33	78.6	285	2 G72415	sensor histidine x
32	33	78.6	355	2 D66436	hypothetical prote
33	33	78.6	403	2 B82496	probable transcrip
34	33	78.6	405	2 F72492	hypothetical prote
35	33	78.6	540	2 UC4916	signal transducing
36	33	78.6	558	2 S57953	CASP protein alpha
37	33	78.6	966	2 G70838	probable mmp11 pr
38	33	78.6	1025	1 DENCED	glutamate dehydrog
39	33	78.6	1192	2 T33157	hypothetical prote
40	33	78.6	2108	2 H70819	probable polykeid
41	32	76.2	92	1 MNWVPM	p10 protein - Orgy
42	32	76.2	92	2 T10402	protein p10 - Orgy
43	32	76.2	100	2 S26728	hypothetical prote
44	32	76.2	119	1 Q0BE23	BLRF3 protein - hu
45	32	76.2	162	2 T07173	hypothetical prote

ALIGNMENTS

RESULT 1

EEWTA
alpha/beta-gliadin precursor - wheat
N/Alternate names: prolamin
C/Species: Triticum aestivum (common wheat)
C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 03-Jul-2004
C/Accession: A03354
R/Rafalski, J.A.; Scheets, K.; Metzler, M.; Peterson, D.M.; Hedgcock, C.; Soll, D.G.
EMBO J. 3, 1409-1415, 1984
A/Title: Developmentally regulated plant genes: the nucleotide sequence of a wheat glia
A/Reference number: A03354; PMID:84261434; PMID:6204862
A/Accession: A03354
A/Molecule type: DNA
A/Residues: 1-286 <RAF>
A/Cross-references: UNIPROT:P02863; GB:X00627; GB:X03076; NID:G21752; PIDN:CA25261.1;
A/Experimental source: cv. Newton
C/Comment: Gliadin is the major seed storage protein in wheat.
C/Superfamily: gliadin
C/Keywords: storage protein; tandem repeat
F/1-20/Domain: signal sequence #status predicted <SIG>
F/16-108/Region: 6-residue repeats ([QP]-Q-Q-P-[FY]-P)
F/21-286/Product: gliadin #status predicted <GIN>
F/116-133/Region: glutamine-rich

Query Match Score 39; DB 1; Length 286;
Best Local Similarity 85.7%; Pred. No. 8.4;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Cy 1 P0PELPY 7
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Db 82 P0PELPY 86

RESULT 2

S07923
alpha/beta-gliadin precursor - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 20-Aug-1999
C/Accession: S07923
R/Sumner-Smith, M.; Rafalski, J.A.; Sugiyama, T.; Stoll, M.; Seel, D.
Nucleic Acids Res. 13, 3905-3916, 1985
A/Title: Conservation and variability of wheat alpha/beta-gliadin genes.
A/Reference number: S07361; PMID:85242077; PMID:3839304
A/Accession: S07923
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-286 <SUM>
A/Cross-references: EMBL:X02539; NID:G21760; PIDN:CA26384.1; PID:G21761
C/Superfamily: gliadin

Query Match Score 39; DB 2; Length 286;
Best Local Similarity 85.7%; Pred. No. 8.4;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POPPLPY 7
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Db 82 POPPLPY 88

RESULT 3

T06498

alpha/beta-gliadin A-II precursor - wheat

G.Species: Triticum aestivum (common wheat)

C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C.Accession: T06498

R.Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A.Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA

A.Reference number: A92541; MUID:85234522; PMID:2989281

A.Accession: T06498

A.Status: translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-291 <OKI>

A.Cross-references: UNIPROT:P04722; EMBL:M10092; NID:G170711; PIDN:AAA34276.1; PID:G1707

C.Superfamily: gliadin

C.Keywords: seed; storage protein

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-291/Product: alpha/beta-gliadin A-II #status predicted <MAT>

Query Match 92.9%; Score 39; DB 2; Length 291;

Best Local Similarity 85.7%; Pred. No. 8.5;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POPPLPY 7
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Db 82 POPPLPY 88

RESULT 4

T06500

alpha/beta-gliadin A-IV precursor - wheat

G.Species: Triticum aestivum (common wheat)

C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C.Accession: T06500

R.Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A.Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA

A.Reference number: A92541; MUID:85234522; PMID:2989281

A.Accession: T06500

A.Status: translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-297 <OKI>

A.Cross-references: UNIPROT:P04724; EMBL:M11075; NID:G170723; PIDN:AAA34282.1; PID:G1707

C.Superfamily: gliadin

C.Keywords: seed; storage protein

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-297/Product: alpha/beta-gliadin A-IV #status predicted <MAT>

Query Match 92.9%; Score 39; DB 2; Length 297;

Best Local Similarity 85.7%; Pred. No. 8.7;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POPPLPY 7
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Db 82 POPPLPY 88

RESULT 5

S10015

alpha/beta-gliadin precursor (clone MM1) - wheat

G.Species: Triticum aestivum (common wheat)

C.Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C.Accession: S10015

R.Garcia-Morero, F.; Marana, C.; Garcia-Olmedo, F.; Carbonero, P.

Plant Mol. Biol. 14, 867-868, 1990

A.Title: Nucleotide sequence of a cDNA encoding an alpha/beta-type gliadin from hexaploid wheat

A.Reference number: S10015; MUID:91346679; PMID:2102865

A.Accession: S10015

A.Molecule type: mRNA

A.Residues: 1-307 <GAR>

A.Cross-references: UNIPROT:P18573; EMBL:X17361; NID:G21672; PIDN:CAA35238.1; PID:G2167

C.Superfamily: gliadin

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-307/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 92.9%; Score 39; DB 2; Length 307;

Best Local Similarity 85.7%; Pred. No. 9.1;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POPPLPY 7
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Db 82 POPPLPY 88

RESULT 6

D22364

alpha/beta-gliadin precursor (clone A735) - wheat

G.Species: Triticum aestivum (common wheat)

C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C.Accession: D22364

R.Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A.Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA

A.Reference number: A92541; MUID:85234522; PMID:2989281

A.Accession: D22364

A.Molecule type: mRNA

A.Residues: 1-326 <OKI>

A.Cross-references: UNIPROT:P04724

C.Superfamily: gliadin

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-326/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 92.9%; Score 39; DB 2; Length 326;

Best Local Similarity 85.7%; Pred. No. 9.7;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 POPPLPY 7
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Db 94 POPPLPY 100

RESULT 7

S45428

PRT112 protein - yeast (Saccharomyces cerevisiae)

N.Alternate names: protein YBL0724; protein YBL080C

C.Species: Saccharomyces cerevisiae

C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C.Accession: S45428; S45821; S41997; S59225; S41792

R.Obermaier, B.; Gassenhuber, J.; Pivrandi, E.; Domdey, H.

submitted to the EMBL Data Library, May 1994

A.Description: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces

A.Reference number: S45387

A.Accession: S45428

A.Molecule type: DNA

A.Residues: 1-541 <DOM>

A.Cross-references: UNIPROT:P33893; EMBL:X79489; NID:G496661; PID:G496701

R.Domdey, H.; Gassenhuber, J.; Obermaier, B.; Pivrandi, E.

submitted to the Protein Sequence Database, August 1994

A.Reference number: S45816

A.Accession: S45821

A.Molecule type: DNA

A.Residues: 1-541 <DOM>

A.Cross-references: EMBL:X79489; NID:G536128; PID:G536129; GSPDB:GN00002; MIPS:YBL080C

R.Domdey, H.; Gassenhuber, J.; Obermaier, B.; Pivrandi, E.

submitted to the Protein Sequence Database, August 1994

A.Reference number: S41997; MUID:94363744; PMID:8082172

A.Accession: S41997

A:Molecule type: DNA
 A:Residues: 1-414, 'P', 416-541 <MTL>
 A:Cross-references: EMBL:112072; NID:9437492; PIDN:ACG37508.1; PID:G347493
 R:Obomater, B.; Gassenhuber, J.; Piravandi, E.; Dornay, H.
 Yeast 11, 1103-1112, 1995
 A:Title: Sequence analysis of a 78.6 kb segment of the left end of *Saccharomyces cerevisiae*
 A:Reference number: S59184; MUID:96076635; PMID:7502586
 A:Accession: S59225
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-541 <OBW>
 A:Cross-references: EMBL:X79489; NID:9496661; PIDN:CAA56028.1; PID:9496701
 A:Note: The nucleotide sequence was submitted to the EMBL Data Library, May 1994
 C:Genetics:
 A:Gene: SGD:PET112; MIPS:YBL080C
 A:Cross-references: SGD:S0000176; MIPS:YBL080C
 A:Map position: 2L
 C:Function:
 A:Description: involved in mitochondrial gene expression, probably in translation
 C:Superfamily: PET112 protein
 C:Keywords: mitochondrion; transmembrane protein
 F:77-93/Domain: transmembrane #status predicted <TMM>

Query Match 88.1%; Score 37; DB 1; Length 541;
 Best Local Similarity 85.7%; Pred. No. 40;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 Db 302 PDPRLPY 308

RESULT 8
 E86537
 Hypothetical protein CPJ0375 [Imported] - *Chlamydomonas reinhardtii* (strain J138)
 C:Species: *Chlamydomonas reinhardtii*, *Chlamydia pneumoniae*
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: E86537
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishida, F.; Ouchi, K.; Shiba, T.; Ishii, T.
 Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of *Chlamydia pneumoniae* J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: E86537
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-165 <STO>
 A:Cross-references: UNIPROT:Q9J5F4; GB:BA000008; NID:96978747; PIDN:BA98583.1; GSPDB:GX
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CPJ0375

Query Match 85.7%; Score 36; DB 2; Length 165;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELRY 7
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 Db 133 PKPELRY 139

RESULT 9
 D72085
 Hypothetical protein CP0381 [Imported] - *Chlamydomonas reinhardtii* (strains CML029 and AR
 C:Species: *Chlamydomonas reinhardtii*, *Chlamydia pneumoniae*
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: D72085; B81582
 R:Salmen, S.; Mitchell, M.; Marache, R.; Lammell, C.; Fan, J.; Olinger, L.; Grimwood, J.;
 Nature Genet. 21, 385-389, 1999
 A:Title: Comparative genomes of *Chlamydia pneumoniae* and *C. trachomatis*.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: D72085
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-165 <ARN>
 A:Cross-references: UNIPROT:Q928G8; GB:AE001622; GB:AE001363; NID:94376652; PIDN:AD1851
 A:Experimental source: strain CML029
 R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of *Chlamydia trachomatis* Mopn and *Chlamydia pneumoniae* AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: B81582
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-165 <REA>
 A:Cross-references: GB:AE002200; GB:AE002161; NID:97189305; PIDN:AAF38228.1; PID:9718930
 A:Experimental source: strain AR39, HL cells
 C:Genetics:
 A:Gene: CPN0375; CP0381

Query Match 85.7%; Score 36; DB 2; Length 165;
 Best Local Similarity 71.4%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 POPELRY 7
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 Db 133 PKPELRY 139

RESULT 10
 S36155
 Paired box protein PAX9 - human
 C:Species: *Homo sapiens* (man)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
 C:Accession: S36155
 R:Stapleton, P.; Welch, A.; Urbanek, P.; Kozmik, Z.; Bueslinger, M.
 Nature Genet. 3, 292-298, 1993
 A:Title: Chromosomal localization of seven PAX genes and cloning of a novel family memb
 A:Reference number: S36155; MUID:95072651; PMID:7981748
 A:Accession: S36155
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-208 <STA>
 A:Cross-references: EMBL:L09745
 C:Genetics:
 A:Gene: GDB:PAX9
 A:Cross-references: GDB:138774; OMIM:167416
 A:Map position: 14q12-14q13
 C:Superfamily: paired box transcription factor Pax-8; paired box homology
 F:2-126/Domain: paired box homology <PBH>

Query Match 85.7%; Score 36; DB 2; Length 208;
 Best Local Similarity 85.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 POPELRY 7
 |||||
 Db 148 PDPALPY 154

RESULT 11
 S57652
 Transcription factor - mouse
 C:Species: *Mus musculus* (house mouse)
 C>Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C:Accession: I48740; I48706; S57652
 R:Neubuser, A.; Koseki, H.; Balling, R.
 Dev. Biol. 170, 701-716, 1995
 A:Title: Characterization and developmental expression of Pax9, a paired-box-containing
 A:Reference number: I48740; MUID:95377555; PMID:7649395
 A:Accession: I48740
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-342 <RRS>
 A:Cross-references: UNIPROT:P47242; EMBL:X64000; NID:9686892; PIDN:CAA58824.1; PID:9896
 R:Wallin, J.; Mizutani, Y.; Imai, K.; Miyashita, N.; Moriwaki, K.; Taniguchi, M.; Koseki

Mamm. Genome 4, 354-358, 1993
 A>Title: A new Pax gene, Pax-9, maps to mouse chromosome 12.
 A/Reference number: 148706; MUID:93364111; PMID:8358189
 A/Accession: 148706
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 19-111 <EE2>
 A/Cross-references: EMBL:X73037; NID:g398815; PIDN:CAA51518.1; PID:g939951

C/Genetics:
 A/Gene: Pax9
 C/Superfamily: paired box transcription factor Pax-8; paired box homology
 F.4.128/Domain: paired box homology <PBH>

Query Match 85.7%; Score 36; DB 2; Length 342;
 Best Local Similarity 85.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELPY 7
 ||| |||
 DB 150 POPALPY 156

RESULT 12

A/Accession: A40023
 Paired box homolog PAX1 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 09-Jul-2004
 C/Accession: A40023
 R/Gallegakis, G.; Fritsch, R.; Fickenscher, H.; Deutsch, U.; Goulding, M.; Gruss, P.
 Cell 66, 873-884, 1991
 A>Title: The molecular basis of the undulated/Pax-1 mutation.
 A/Reference number: A40023; MUID:91364170; PMID:1889089
 A/Accession: A40023
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-361 <CHA>
 A/Cross-references: UNIPROT:P09084; GB:M69222; NID:g200223; PIDN:AAA39868.1; PID:g200224
 C/Superfamily: paired box transcription factor Pax-8; paired box homology
 C/Keywords: DNA binding; transcription regulation
 F.4.128/Domain: paired box homology <PBH>

Query Match 85.7%; Score 36; DB 2; Length 361;
 Best Local Similarity 85.7%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELPY 7
 ||| |||
 DB 148 POPALPY 154

RESULT 13

A/Accession: T52354
 Hypothetical protein B1E6.30 [imported] - Neurospora crassa
 C/Species: Neurospora crassa
 C/Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
 C/Accession: T52354
 R/Schulte, U.; Aign, V.; Hohelsel, U.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, B.
 Submitted to the Protein Sequence Database, September 2000
 A/Reference number: Z26053
 A/Accession: T52354
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-289 <SCH>
 A/Cross-references: UNIPROT:Q9HRU3; EMBL:AL42043; GSPDB:GN00116; NCSP:B1E6.30
 A/Experimental source: BAC clone B1E6; strain OR74A
 C/Genetics:
 A/Gene: NCSP:B1E6.30
 A/Map position: 6

Query Match 83.3%; Score 35; DB 2; Length 289;
 Best Local Similarity 71.4%; Pred. No. 46;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELPY 7
 ||| |||
 DB 188 POPSLPY 194

RESULT 14

A/Accession: G96014
 Hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSym
 C/Species: Sinorhizobium meliloti
 C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C/Accession: G96014
 R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hema
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A>Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing end
 A/Reference number: A95842; MUID:21396508; PMID:11481431
 A/Accession: G96014
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-306 <KUR>
 A/Cross-references: UNIPROT:Q92TW2; GB:AL591985; PIDN:CAC49783.1; PID:G15141270; GSPDB:
 A/Experimental source: strain 1021, megaplasmid pSymB
 R/Galbert, F.; Finan, T.M.; Long, S.R.; Punher, A.; Abola, P.; Ampe, F.; Barley-Huber
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Leisner
 hehault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Ye
 A>Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A/Reference number: A96039; MUID:21368234; PMID:11474104
 A/Contents: annotation
 C/Genetics:
 A/Gene: SMD20676
 A/Genome: plasmid

Query Match 83.3%; Score 35; DB 2; Length 306;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELPY 6
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 DB 85 POPELPY 90

RESULT 15

A/Accession: T20107
 Hypothetical protein CS0P4.10 - Caenorhabditis elegans
 C/Species: Caenorhabditis elegans
 C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C/Accession: T20107
 R/McMurray, A.
 Submitted to the EMBL Data Library, April 1996
 A/Reference number: Z19225
 A/Accession: T20107
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-332 <WIL>
 A/Cross-references: UNIPROT:Q15738; EMBL:Z70750; PIDN:CAA94735.1; GSPDB:GN00023; CESB:
 A/Experimental source: clone CS0P4
 C/Genetics:
 A/Gene: CESP:CS0P4.10
 A/Map position: 5
 A/Introns: 75/3; 120/3; 193/3; 303/3
 C/Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 83.3%; Score 35; DB 2; Length 332;
 Best Local Similarity 85.7%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELPY 7
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 DB 313 POPELPY 319

Wed Dec 15 10:01:54 2004

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Job time : 15.7083 secs

us-10-089-700-1.rpr

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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07 ; Search time 15.75 Seconds
(without alignments)
29.475 Million cell updates/sec

Title: US-10-089-700-1

Perfect score: 42

Sequence: 1 PQEPLPY 7

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Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	92.9	242	4	US-09-270-767-61492
2	39	92.9	790	4	US-09-270-767-45954
3	36	85.7	168	4	US-09-198-452A-391
4	36	85.7	246	4	US-09-248-796A-23501
5	36	85.7	337	4	US-08-930-830B-2
6	36	85.7	342	4	US-08-930-830B-5
7	35	83.3	67	4	US-09-270-767-61826
8	35	83.3	110	4	US-09-270-767-40381
9	35	83.3	110	4	US-09-270-767-55597
10	35	83.3	170	4	US-09-252-991A-23935
11	35	83.3	386	4	US-09-270-767-46258
12	35	83.3	450	2	US-08-611-280-25
13	35	83.3	450	3	US-09-195-940-25
14	35	83.3	450	3	US-09-562-466-25
15	35	83.3	451	3	US-08-654-482-14
16	35	83.3	745	4	US-09-710-279-1742
17	35	83.3	746	2	US-08-785-431-4
18	35	83.3	746	2	US-09-205-048-4
19	35	83.3	788	2	US-08-785-431-2
20	35	83.3	798	3	US-09-205-048-2
21	35	83.3	798	3	US-09-134-001C-4917
22	35	83.3	1053	4	US-09-252-991A-26140
23	34	81.0	494	4	US-09-543-681A-7142
24	33	78.6	54	3	US-08-301-162-12
25	33	78.6	54	3	US-09-461-240-12
26	33	78.6	54	3	US-09-968-927-12
27	33	78.6	118	4	US-09-489-039A-12813

28	33	78.6	213	3	US-08-911-853-13	Sequence 13, Appl
29	33	78.6	213	3	US-09-479-409-13	Sequence 13, Appl
30	33	78.6	213	3	US-09-479-453-13	Sequence 13, Appl
31	33	78.6	267	3	US-08-301-162-16	Sequence 16, Appl
32	33	78.6	267	3	US-09-461-240-15	Sequence 16, Appl
33	33	78.6	267	4	US-09-968-927-15	Sequence 16, Appl
34	33	78.6	321	4	US-09-328-352-6269	Sequence 6269, Ap
35	33	78.6	398	3	US-09-303-064-54	Sequence 54, Appl
36	33	78.6	398	3	US-09-086-503-54	Sequence 54, Appl
37	33	78.6	568	3	US-09-188-930-291	Sequence 291, App
38	33	78.6	568	4	US-09-312-283C-291	Sequence 291, App
39	33	78.6	811	4	US-09-248-796A-16439	Sequence 16439, A
40	33	78.6	1590	4	US-09-617-099B-1	Sequence 1, Appl
41	32	76.2	69	4	US-09-248-796A-14211	Sequence 14211, A
42	32	76.2	85	4	US-09-634-238-316	Sequence 316, App
43	32	76.2	127	4	US-09-198-452A-1034	Sequence 1034, Ap
44	32	76.2	138	4	US-09-270-767-57185	Sequence 57185, A
45	32	76.2	209	4	US-09-270-767-41935	Sequence 41935, A

ALIGNMENTS

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RESULT 1
US-09-270-767-61492
; Sequence 61492, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61492
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-61492

Query Match          92.9%; Score 39; DB 4; Length 242;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      1  PQEPLPY 7
Db      232 PQEPLPY 238

RESULT 2
US-09-270-767-45954
; Sequence 45954, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45954
; LENGTH: 790
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-45954

Query Match          92.9%; Score 39; DB 4; Length 790;

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Best Local Similarity 85.7%; Pred. No. 91;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPPLPY 7
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DB 330 POPPLPY 336

RESULT 3
US-09-198-452A-391

Sequence 391, Application US/09198452A
Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

PRIOR FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 391

LENGTH: 168

TYPE: PRT

ORGANISM: Chlamydia pneumoniae

FEATURE:

NAME/KEY: SITE

LOCATION: 1..168

OTHER INFORMATION: Xaa=unknown or other

US-09-198-452A-391

Query Match

Best Local Similarity 85.7%; Score 36; DB 4; Length 168;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPPLPY 7
|||:|
DB 136 PKPEIPY 142

RESULT 4
US-09-248-796A-23501

Sequence 23501, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 23501

LENGTH: 246

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-23501

Query Match

Best Local Similarity 85.7%; Score 36; DB 4; Length 246;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPPLPY 7
|||:|
DB 175 PTPPLPY 181

RESULT 5
US-08-930-830B-2

Sequence 2, Application US/08930830B
Patent No. 6514712

GENERAL INFORMATION:

APPLICANT: Peters, Heiko

APPLICANT: Balling, Rudolf

APPLICANT: Hofer, Heinz

APPLICANT: Richter, Thomas

TITLE OF INVENTION: No. 6514712el probe for early diagnosis of epithelial dysplasias of the stratified squamous epithelium and for

TITLE OF INVENTION: tumour diagnosis and tumour therapy of squamous epithelial

TITLE OF INVENTION: carcinomas

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.

STREET: 1100 No. 6514712th Glebe Rd. 8th floor

CITY: Arlington

STATE: VA

COUNTRY: USA

ZIP: 22201-4741

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/930,830B

FILING DATE: 16-JAN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP97/00564

FILING DATE: 07-FEB-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 19605105.3

FILING DATE: 12-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: Sadroff, B.J.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 2861-6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4000

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 337 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-930-830B-2

QY 1 POPPLPY 7
|||:|
DB 148 POPPLPY 154

RESULT 6
US-08-930-830B-5

Sequence 5, Application US/08930830B

Patent No. 6514712

GENERAL INFORMATION:

APPLICANT: Peters, Heiko

APPLICANT: Balling, Rudolf

APPLICANT: Hofer, Heinz

APPLICANT: Richter, Thomas

TITLE OF INVENTION: No. 6514712el probe for early diagnosis of epithelial

TITLE OF INVENTION: dysplasias of the stratified squamous epithelium and for

TITLE OF INVENTION: tumour diagnosis and tumour therapy of squamous epithelial

TITLE OF INVENTION: carcinomas

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHAYE P.C.


```
STREET: 1100 No. 6514712th Glebe Rd. 8th floor
CITY: Arlington
STATE: VA
COUNTRY: USA
ZIP: 22201-4741
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,830B
FILING DATE: 16-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP97/00564
FILING DATE: 07-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 19605105.3
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sadhoff, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2861-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-830B-5

Query Match
Best Local Similarity 85.7%; Score 36; DB 4; Length 342;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELP 7
DB 150 POPALPY 156

RESULT 7
US-09-270-767-61826
Sequence 61826, Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 61826
LENGTH: 67
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-61826

Query Match
Best Local Similarity 83.3%; Score 35; DB 4; Length 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELP 6
DB 13 POPALPY 18

RESULT 8
US-09-270-767-40381
Sequence 40381, Application US/09270767
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Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 40381
LENGTH: 110
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-40381

Query Match
Best Local Similarity 83.3%; Score 35; DB 4; Length 110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELP 6
DB 94 POPALPY 99

RESULT 9
US-09-270-767-55597
Sequence 55597, Application US/09270767
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 55597
LENGTH: 110
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55597

Query Match
Best Local Similarity 83.3%; Score 35; DB 4; Length 110;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELP 6
DB 94 POPALPY 99

RESULT 10
US-09-252-991A-23935
Sequence 23935, Application US/09252991A
GENERAL INFORMATION:
APPLICANT: Marc J. Rubinfeld et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196, 136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23935
LENGTH: 170
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23935

Query Match
Best Local Similarity 83.3%; Score 35; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELP 6
DB 152 POPELP 157

RESULT 11
US-09-270-767-46258
Sequence 46258, Application US/09270767

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
NUMBER OF SEQ ID NOS: 1999-03-17
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 46258
LENGTH: 386
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-46258

Query Match
Best Local Similarity 83.3%; Score 35; DB 4; Length 386;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPELP 6
DB 13 POPELP 18

RESULT 12
US-08-611-280-25

Sequence 25, Application US/08611280
Patent No. 5891666
GENERAL INFORMATION:

APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6G7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-611-280-25

Query Match
Best Local Similarity 83.3%; Score 35; DB 2; Length 450;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELPY 7
DB 185 PHEPIPY 191

RESULT 13
US-09-195-940-25
Sequence 25, Application US/09195940

GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTRY: Canada
ZIP: L5N 6G7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/195,940
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/611,280
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-195-940-25

Query Match
Best Local Similarity 83.3%; Score 35; DB 3; Length 450;
Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 POPELPY 7
DB 185 PHEPIPY 191

RESULT 14

US-09-562-466-25
Sequence 25, Application US/09562466
Patent No. 6369202
GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
Grossman, Alex

Richardson, Christopher D
 TITLE OF INVENTION: NOVEL GENES ENCODING LIRF POLYPEPTIDES
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Amgen Canada Inc.
 STREET: 6733 Mississauga Road, Suite 303
 CITY: Mississauga
 STATE: Ontario
 COUNTRY: Canada
 ZIP: L5N 6U8
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/562,466
 FILING DATE: 01-May-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/195,940
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Oleski, Nancy A.
 REGISTRATION NUMBER: 34,688
 REFERENCE/DOCKET NUMBER: A-338A
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 US-09-562-466-25

Query Match 83.3%; Score 35; DB 3; Length 450;
 Best Local Similarity 71.4%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 P0PELPY 7
 Db 186 PHELPY 191

RESULT 15
 US-08-654-482-14
 Sequence 14, Application US/08654482
 Patent No. 6245562
 GENERAL INFORMATION:
 APPLICANT: Dalla-Favera, Riccardo
 TITLE OF INVENTION: IDENTIFICATION OF GENES ALTERED IN
 TITLE OF INVENTION: MULTIPLE MYELOMA
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/654,482
 FILING DATE: 28-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 50995
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 278-0400
 TELEFAX: (212) 391-0525
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 451 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-654-482-14

Query Match 83.3%; Score 35; DB 3; Length 451;
 Best Local Similarity 71.4%; Pred. No. 2.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 P0PELPY 7
 Db 186 PHELPY 192

Search completed: December 14, 2004, 17:00:56
 Job time : 16.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07 ; Search time 58.333 Seconds

(without alignments)
42.861 Million cell updates/sec

Title: US-10-089-700-1

Perfect score: 42

Sequence: 1 P0PELPY 7

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	42	100.0	12	US-10-367-405-14
2	42	100.0	13	US-10-367-405-17
3	42	100.0	14	US-10-367-405-15
4	42	100.0	14	US-10-367-405-18
5	39	92.9	9	US-10-367-405-20
6	39	92.9	9	US-10-367-405-21
7	39	92.9	9	US-10-367-405-22
8	39	92.9	10	US-10-367-405-10
9	39	92.9	11	US-10-367-405-6
10	39	92.9	12	US-10-367-405-1
11	39	92.9	12	US-10-367-405-2
12	39	92.9	12	US-10-474-955-15
13	39	92.9	12	US-10-474-955-20

ALIGNMENTS

RESULT 1
US-10-367-405-14
Sequence 14, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:
APPLICANT: Felix Hausch
APPLICANT: Ian Shan
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-238US1
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/357,238
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/380,761
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/392,782
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/422,933
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 60/428,033
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: 60/435,881
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 12
TYPE: PRT
ORGANISM: triticum aestivum
US-10-367-405-14
Query Match 100.0%; Score 42; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

best dates found

QY 1 POPELPHY 7
|||||
DB 6 POPELPHY 12

RESULT 2

US-10-367-405-17
Sequence 17, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:

APPLICANT: Felix Hausch
APPLICANT: Gary Gray

APPLICANT: Chaitan Khosla
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1

CURRENT FILING DATE: 2003-02-14
CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-10-31
PRIOR FILING DATE: 2002-10-31

PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 13
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-367-405-17

Query Match 100.0%; Score 42; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.3; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;

QY 1 POPELPHY 7
|||||
DB 1 POPELPHY 7

RESULT 3

US-10-367-405-15
Sequence 15, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:

APPLICANT: Felix Hausch
APPLICANT: Gary Gray

APPLICANT: Chaitan Khosla
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1

CURRENT FILING DATE: 2003-02-14
CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-10-31
PRIOR FILING DATE: 2002-10-31

PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 14
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-367-405-15

NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 14
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-367-405-15

Query Match 100.0%; Score 42; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;

QY 1 POPELPHY 7
|||||
DB 1 POPELPHY 7

RESULT 4

US-10-367-405-18
Sequence 18, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:

APPLICANT: Felix Hausch
APPLICANT: Gary Gray

APPLICANT: Chaitan Khosla
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1

CURRENT FILING DATE: 2003-02-14
CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14

PRIOR FILING DATE: 2002-05-14
PRIOR FILING DATE: 2002-05-14

PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-10-31
PRIOR FILING DATE: 2002-10-31

PRIOR FILING DATE: 2002-11-20
PRIOR FILING DATE: 2002-11-20

NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 18
LENGTH: 14
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-367-405-18

Query Match 100.0%; Score 42; DB 14; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.5; Mismatches 0; Gaps 0;

Matches 7; Conservative 0; Indels 0; Gaps 0;

QY 1 POPELPHY 7
|||||
DB 1 POPELPHY 7

RESULT 5

US-10-367-405-20
Sequence 20, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:

APPLICANT: Felix Hausch
APPLICANT: Gary Gray

APPLICANT: Chaitan Khosla
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1

CURRENT FILING DATE: 2003-02-14
CURRENT FILING DATE: 2003-02-14

PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 14
TYPE: PRT
ORGANISM: Trilicium aestivum
US-10-367-405-20

Wed Dec 15 10:01:54 2004

us-10-089-700-1.rapb

Page 3

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; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T cell epitope
US-10-367-405-20
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Query Match      92.9%; Score 39; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0;
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Qy 1 POPOLPY 7
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Db 3 POPOLPY 9
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RESULT 6
US-10-367-405-21
; Sequence 21, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T cell epitope
US-10-367-405-21
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```

Query Match      92.9%; Score 39; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 POPOLPY 7
    |||:||||
Db 1 POPOLPY 7
```

```

RESULT 7
US-10-367-405-22
; Sequence 22, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T cell epitope
US-10-367-405-22
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```

Query Match      92.9%; Score 39; DB 14; Length 9;
Best Local Similarity 85.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 POPOLPY 7
    |||:||||
Db 3 POPOLPY 9
```

```

RESULT 8
US-10-367-405-10
; Sequence 10, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
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LENGTH: 10
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-367-405-10

Query Match 92.9%; Score 39; DB 14; Length 10;
Best Local Similarity 85.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPOLPY 7
|||:||||
DB 4 POPOLPY 10

RESULT 9
US-10-367-405-6
Sequence 6, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:
APPLICANT: Felix Hausch
APPLICANT: Gary Gray
APPLICANT: Lu Shan
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1
CURRENT APPLICATION NUMBER: US/10/367,405
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/357,238
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/380,761
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/392,782
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/422,933
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 60/428,033
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: 60/435,881
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-367-405-6

Query Match 92.9%; Score 39; DB 14; Length 11;
Best Local Similarity 85.7%; Pred. No. 6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPOLPY 7
|||:||||
DB 5 POPOLPY 11

RESULT 10
US-10-367-405-1
Sequence 1, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:
APPLICANT: Felix Hausch
APPLICANT: Gary Gray
APPLICANT: Lu Shan
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1
CURRENT APPLICATION NUMBER: US/10/367,405
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/357,238
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/380,761
PRIOR FILING DATE: 2002-05-14

Query Match 92.9%; Score 39; DB 14; Length 12;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPOLPY 7
|||:||||
DB 6 POPOLPY 12

RESULT 12
US-10-474-955-15

PRIOR APPLICATION NUMBER: 60/392,782
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/422,933
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 60/428,033
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: 60/435,881
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-367-405-1

Query Match 92.9%; Score 39; DB 14; Length 12;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPOLPY 7
|||:||||
DB 6 POPOLPY 12

RESULT 11
US-10-367-405-2
Sequence 2, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:
APPLICANT: Felix Hausch
APPLICANT: Gary Gray
APPLICANT: Lu Shan
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1
CURRENT APPLICATION NUMBER: US/10/367,405
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/357,238
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/380,761
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/392,782
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/422,933
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 60/428,033
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: 60/435,881
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 12
TYPE: PRT
ORGANISM: Triticum aestivum
FEATURE: PYROGLUTAMINE CAR
NAME/KEY: (1)...(1)
LOCATION: (1)...(1)
OTHER INFORMATION: N terminal pyroglutamate
US-10-367-405-2

Query Match 92.9%; Score 39; DB 14; Length 12;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 POPOLPY 7
|||:||||
DB 6 POPOLPY 12

RESULT 12
US-10-474-955-15


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; Sequence 15, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifflough, Jan W.
; APPLICANT: Konig, Fritz
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS A
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope G11a-ALPHA9 (57-68)
US-10-474-955-15

```

```

Query Match          92.9%; Score 39; DB 17; Length 12;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 POPELPHY 7
    |||:||||
DB 6 POPOLPHY 12

```

```

RESULT 13
US-10-474-955-20
; Sequence 20, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifflough, Jan W.
; APPLICANT: Konig, Fritz
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS A
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope DQ2-ALPHA-III
US-10-474-955-20

```

```

Query Match          92.9%; Score 39; DB 17; Length 12;
Best Local Similarity 85.7%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 POPELPHY 7
    |||:||||
DB 6 POPOLPHY 12

```

```

RESULT 14
US-10-367-405-4
; Sequence 4, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
US-10-367-405-4

```

```

; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-4

```

```

Query Match          92.9%; Score 39; DB 14; Length 13;
Best Local Similarity 85.7%; Pred. No. 7.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 POPELPHY 7
    |||:||||
DB 1 POPOLPHY 7

```

```

RESULT 15
US-10-367-405-3
; Sequence 3, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Gary Gray
; APPLICANT: Felix Hausch
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-3

```

```

Query Match          92.9%; Score 39; DB 14; Length 14;
Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 POPELPHY 7
    |||:||||
DB 1 POPOLPHY 7

```

Wed Dec 15 10:01:54 2004

Search completed: December 14, 2004, 17:09:34
Job time : 59.333 secs

us-10-089-700-1.rapb

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07 ; Search time 178.5 Seconds
(without alignments)
54.798 Million cell updates/sec

Title: US-10-089-700-2
Perfect score: 97
Sequence: 1 QLOPFPQPLPYPOQ 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	92.8	290	2	Q9M4L6
2	90	92.8	291	1	Q9M4L6
3	90	92.8	297	1	Q9M4L6
4	90	92.8	307	1	Q9M4L6
5	86	88.7	273	2	Q9M4M4
6	82	84.5	259	2	Q9M4L7
7	82	84.5	269	2	Q9M4L7
8	82	84.5	270	2	Q9M4L7
9	82	84.5	274	1	Q9M4M5
10	82	84.5	286	1	Q9M4L6
11	82	84.5	286	1	Q9M4L6
12	82	84.5	287	2	Q9M4L6
13	82	84.5	288	2	Q9M4L6
14	82	84.5	289	2	Q9M4L6
15	82	84.5	318	2	Q9M4L6
16	81.5	84.0	313	1	Q9M4L6
17	81.5	84.0	313	2	Q9M4L6
18	81.5	84.0	313	2	Q9M4L6
19	81.5	84.0	319	1	Q9M4L6
20	80	82.5	277	2	Q9M4L6
21	74	76.3	276	2	Q9M4M2
22	74	76.3	276	2	Q9M4M2
23	74	76.3	278	2	Q9M4M2
24	74	76.3	288	2	Q9M4M2
25	72.5	74.7	296	1	Q9M4L6
26	72.5	74.7	296	2	Q9M4L6
27	72	74.2	262	1	Q9M4L6
28	72	74.2	287	2	Q9M4L6
29	66.5	68.6	347	2	Q9M4L6
30	65	67.0	280	2	Q9M4L6
31	65	67.0	392	2	Q9M4L6

32	63.5	65.5	265	2	Q9M4M3	Q9M4M3	tritricum ae
33	63.5	65.5	265	2	Q9M4M6	Q9M4M6	tritricum ae
34	63.5	65.5	282	1	Q9M4L6	Q9M4L6	tritricum ae
35	63	64.9	192	2	Q9M4L6	Q9M4L6	tritricum ur
36	63	64.9	192	2	Q9M4L6	Q9M4L6	tritricum ur
37	63	64.9	194	2	Q9M4L6	Q9M4L6	tritricum ur
38	63	64.9	203	2	Q9M4L6	Q9M4L6	tritricum ur
39	63	64.9	213	2	Q9M4L6	Q9M4L6	tritricum ur
40	63	64.9	239	2	Q9M4L6	Q9M4L6	tritricum ur
41	63	64.9	274	2	Q9M4L6	Q9M4L6	tritricum ur
42	63	64.9	279	2	Q9M4L6	Q9M4L6	tritricum ur
43	63	64.9	280	2	Q9M4L6	Q9M4L6	tritricum ur
44	63	64.9	280	2	Q9M4L6	Q9M4L6	tritricum ur
45	63	64.9	282	2	Q9M4L6	Q9M4L6	tritricum ur

ALIGNMENTS

```

RESULT 1
Q9M4L6 PRELIMINARY; PRT; 290 AA.
ID Q9M4L6
AC Q9M4L6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-glutinin.
OS Tritricum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
CX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mjoelner, TISSUE=Endosperm;
RA Arendz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
RL Solid L.M.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133612; CAB76964.1; ...
DR GO; GO:0045735; Functional reservoir activity; IEA.
DR InterPro; IPR003612; AAT.
DR InterPro; IPR001376; Gliadin.
DR Pfam; PF00234; Tryp_alpha_amyl; 1.
DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAT; 1.
FT CHAIN
FT SEQUENCE 290 AA; 33735 MW; C47370FA69FE0BE4 CRC64;

Query Match 92.8%; Score 90; DB 2; Length 290;
Best Local Similarity 93.8%; Pred. No. 0.00061;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Q9M4L6 1 QLOPFPQPLPYPOQ 16
Db 58 QLOPFPQPLPYPOQ 73

RESULT 2
Q9M4L6 STANDARD; PRT; 291 AA.
ID Q9M4L6
AC Q9M4L6;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 29-MAR-2004 (Rel. 43, Last annotation update)
DE Alpha/beta-gliadin A-II precursor (Prolamin).
OS Tritricum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
CX NCBI_TaxID=4565;
RN [1]

```

RP SEQUENCE FROM N.A.
 RX MEDLINE=85234522; PubMed=2989281;
 RA Orita T.W., Cheesbrough V., Reeves C.D.;
 RT "Evolution and heterogeneity of the alpha-/beta-type and gamma-type
 RL gliadin DNA sequences";
 RL J. Biol. Chem. 260:8203-8213(1985).
 CC -1- FUNCTION: Gliadin is the major seed storage protein in wheat.
 CC -1- PFM: Substrate of transglutaminase (By similarity).
 CC -1- ALLERGEN: Causes an allergic reaction in human. Is the cause of
 CC the celiac disease, also known as celiac sprue or gluten-sensitive
 CC enteropathy (By similarity).
 CC -1- MISCELLANEOUS: The alpha/beta-gliadins can be divided into 5
 CC homology classes. Sequence divergence between the classes is due
 CC to single base substitutions and to duplications or deletions
 CC within or near direct repeats. There are more than a 100 copies of
 CC the gene for alpha/beta-gliadin per haploid genome.
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 CC -----
 DR SML; M10092; AAA34276.1; -.
 DR PIR; C22364; C22364.
 DR PIR; T06498; T06498.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; GliA glutenn.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00208; GLIADSLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 DR Allergen; Multigene family; Repeat; Seed storage protein; Signal.
 FT SIGNAL
 FT CHAIN 1 20 Alpha/beta-gliadin A-II.
 SQ SEQUENCE 291 AA; 33661 MW; 9B39P93B0825A280 CRC64;
 Query Match 92.8%; Score 90; DB 1; Length 291;
 Best Local Similarity 93.8%; Pred. No. 0.00061;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 QLOPPQPELPYPOQ 16
 Db 77 QLOPPQPELPYPOQ 92
 RESULT 3
 GDA4 WHEAT STANDARD; PRT; 297 AA.
 ID GDA4 WHEAT STANDARD; PRT; 297 AA.
 AC P04724;
 RT 13-AUG-1987 (Rel. 05, Created)
 RT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha/beta-gliadin A-IV precursor (Prolamin).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 NC NCB1_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85234522; PubMed=2989281;
 RA Orita T.W., Cheesbrough V., Reeves C.D.;
 RT "Evolution and heterogeneity of the alpha-/beta-type and gamma-type
 RL gliadin DNA sequences";
 RL J. Biol. Chem. 260:8203-8213(1985).
 CC -1- FUNCTION: Gliadin is the major seed storage protein in wheat.
 CC -1- PFM: Substrate of transglutaminase (By similarity).
 CC -1- ALLERGEN: Causes an allergic reaction in human. Is the cause of
 CC the celiac disease, also known as celiac sprue or gluten-sensitive

CC enteropathy (By similarity).
 CC -1- MISCELLANEOUS: The alpha/beta-gliadins can be divided into 5
 CC homology classes. Sequence divergence between the classes is due
 CC to single base substitutions and to duplications or deletions
 CC within or near direct repeats. There are more than a 100 copies of
 CC the gene for alpha/beta-gliadin per haploid genome.
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 CC -----
 DR SML; M1075; AAA34282.1; -.
 DR PIR; D22364; D22364.
 DR PIR; T06500; T06500.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; GliA glutenn.
 DR Pfam; PF00234; Tryp alpha amyl; 1.
 DR PRINTS; PR00208; GLIADSLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 DR Allergen; Multigene family; Repeat; Seed storage protein; Signal.
 FT SIGNAL
 FT CHAIN 1 20 Alpha/beta-gliadin A-IV.
 SQ SEQUENCE 297 AA; 34239 MW; 0025ED289AB588B CRC64;
 Query Match 92.8%; Score 90; DB 1; Length 297;
 Best Local Similarity 93.8%; Pred. No. 0.00063;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 QLOPPQPELPYPOQ 16
 Db 77 QLOPPQPELPYPOQ 92
 RESULT 4
 GDA9 WHEAT STANDARD; PRT; 307 AA.
 ID GDA9 WHEAT STANDARD; PRT; 307 AA.
 AC P18573;
 RT 01-NOV-1990 (Rel. 16, Created)
 RT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 29-MAR-2004 (Rel. 43, Last annotation update)
 DE Alpha/beta-gliadin MM1 precursor (Prolamin).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 NC NCB1_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese Spring; TISSUE=Endosperm;
 RX MEDLINE=91346679; PubMed=2102865;
 RA Garcia-Maroto F., Manana C., Garcia-Olmedo F., Carbonero P.;
 RT "Nucleotide sequence of a cDNA encoding an alpha/beta-type gliadin
 RT from hexaploid wheat (Triticum aestivum).";
 RL Plant Mol. Biol. 14:867-868(1990).
 RN [2]
 RP ALLERGENICITY.
 RX PubMed=12351792; DOI=10.1126/science.1074129;
 RA Shan L., Molberg O., Parrot I., Hausch F., Filiz F., Gray G.M.,
 RA Solid L.M., Khosla C.;
 RT "Structural basis for gluten intolerance in celiac sprue";
 RL Science 297:2275-2279(2002).
 CC -1- FUNCTION: Gliadin is the major seed storage protein in wheat.
 CC -1- PFM: Substrate of transglutaminase.
 CC -1- ALLERGEN: Causes an allergic reaction in human. Is the cause of
 CC the celiac disease, also known as celiac sprue or gluten-sensitive
 CC enteropathy.
 CC -1- MISCELLANEOUS: An internal 33-mer peptide seems to be the primary

```

CC CC      Initiator of the inflammatory response to gluten.
CC CC      -1- MISCELLANEOUS: The alpha/beta-gliadins can be divided into 5
CC CC      homology classes. Sequence divergence between the classes is due
CC CC      to single base substitutions and to duplications or deletions
CC CC      within or near direct repeats. There are more than a 100 copies of
CC CC      the gene for alpha/beta-gliadin per haploid genome.
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CC CC      or send an email to license@isb-sib.ch).
CC CC      -----
DR DR      EMBL, X17361, CA935238.1; -.
DR DR      PIR, S10015, S10015.
DR DR      InterPro: IPR003612; AAI.
DR DR      InterPro: IPR001376; Gliadin.
DR DR      InterPro: IPR001954; GliA_gluTenin.
DR DR      Pfam: PF00234; TYP_alpha_amy1. 1.
DR DR      PRINTS: PR00208; GLIADGUTEN.
DR DR      PRINTS: PR00209; GLIADIN.
DR DR      SMART; SM00499; AAI; 1.
DR DR      Allergen; Multigene family; Repeat; Seed storage protein; Signal.
FT FT      SIGNAL 1 20
FT CHAIN 1 307 Alpha/beta-gliadin MW1.
SQ SEQUENCE 307 AA; 35397 MW; 06C1858BD956F1E08 CRC64;

Query Match 92.8%; Score 90; DB 1; Length 307;
Best Local Similarity 93.8%; Pred. No. 0.00065;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPPPOPELPYPOPO 16
DB 77 QLOPPPOPELPYPOPO 92

RESULT 5
Q9M4M4 PRELIMINARY; PRT; 273 AA.
ID Q9M4M4
AC Q9M4M4.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-gliadin.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mjoeiner; TISSUE=Endosperm;
RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
RA Sollid L.W.,
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133604; CAB76956.1; -.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro: IPR003612; AAI.
DR InterPro: IPR001376; GliA_gluTenin.
DR InterPro: IPR001954; GliA_gluTenin.
DR Pfam; PF00234; TYP_alpha_amy1. 1.
DR PRINTS; PR00208; GLIADGUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAI; 1.
FT CHAIN 1 273 alpha-gliadin.
SQ SEQUENCE 273 AA; 31953 MW; 1518E4FF727BDBF1 CRC64;

Query Match 88.7%; Score 86; DB 2; Length 273;
Best Local Similarity 87.5%; Pred. No. 0.0019;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 QLOPPPOPELPYPOPO 16
DB 58 QLOPPPOPELPYPOPO 73

RESULT 6
Q41533 PRELIMINARY; PRT; 259 AA.
ID Q41533
AC Q41533.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-gliadin (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98409296; PubMed=9738916;
RA Maruyama N., Ichise K., Katsube T., Kishimoto T., Kawase S.,
RA Matsumura Y., Takeuchi Y., Sawada T., Utsuni S.,
RT "Identification of major wheat allergens by means of the Escherichia
RT coli expression system."
RL Eur. J. Biochem. 255:739-745(1998).
DR EMBL; D84341; BAA12318.1; -.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro: IPR003612; AAI.
DR InterPro: IPR001376; Gliadin.
DR InterPro: IPR001954; GliA_gluTenin.
DR Pfam; PF00234; TYP_alpha_amy1. 1.
DR PRINTS; PR00208; GLIADGUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAI; 1.
FT NON TER 1 1
FT CHAIN <1 259 alpha-gliadin mature peptide.
SQ SEQUENCE 259 AA; 29996 MW; FE36CD48FD8F54C6 CRC64;

Query Match 84.5%; Score 82; DB 2; Length 259;
Best Local Similarity 87.5%; Pred. No. 0.006;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPPPOPELPYPOPO 16
DB 57 QLOPPPOPELPYPOPO 72

RESULT 7
Q9M4L7 PRELIMINARY; PRT; 269 AA.
ID Q9M4L7
AC Q9M4L7.
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha-gliadin.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mjoeiner; TISSUE=Endosperm;
RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
RA Sollid L.W.,
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ133611; CAB76963.1; -.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro: IPR003612; AAI.
DR InterPro: IPR001376; GliA_gluTenin.
DR InterPro: IPR001954; GliA_gluTenin.
DR Pfam; PF00234; TYP_alpha_amy1. 1.

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DR PRINTS; PR00208; GIADGLUTEN.
 DR SMART; PR00209; GIADIN.
 DR SMART; SM00499; AAI; 1.
 FT CHAIN 1 269 alpha-gliadin.
 SQ SEQUENCE 269 AA; 31292 MW; 87127D6FD15EC78B CRC64;

Query Match 84.5%; Score 82; DB 2; Length 269;
 Best Local Similarity 87.5%; Pred. No. 0.0063;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 QLOPFPQPELPYPOQ 16
 58 QLOPFPQPELPYPOQ 73

RESULT 8

Q9M419 PRELIMINARY; PRT; 270 AA.

DR Q9M419
 AC Q9M419
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-MAR-2004 (TREMUREL. 26, Last annotation update)
 DE Alpha-gliadin.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Mjoeiner; TISSUE=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Solid L.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ133603; CAB76951.1; F:nutrient reservoir activity; IEA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001376; Gliadin.
 DR Pfam; PF00234; TYP alpha amy1; 1.
 DR PRINTS; PR00208; GIADGLUTEN.
 DR PRINTS; PR00209; GIADIN.
 DR SMART; SM00499; AAI; 1.
 FT CHAIN 1 270 alpha-gliadin.
 SQ SEQUENCE 270 AA; 31491 MW; 1DB46528EFADEF5 CRC64;

Query Match 84.5%; Score 82; DB 2; Length 270;
 Best Local Similarity 87.5%; Pred. No. 0.0063;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 QLOPFPQPELPYPOQ 16
 58 QLOPFPQPELPYPOQ 73

RESULT 9

Q9M419 PRELIMINARY; PRT; 274 AA.

DR Q9M419
 AC Q9M419
 DT 01-OCT-2000 (TREMUREL. 15, Created)
 DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
 DT 01-MAR-2004 (TREMUREL. 26, Last annotation update)
 DE Alpha-gliadin.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Mjoeiner; TISSUE=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Solid L.M.;

RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133603; CAB76951.1; F:nutrient reservoir activity; IEA.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR001376; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001376; Gliadin.
 DR Pfam; PF00234; TYP alpha amy1; 1.
 DR PRINTS; PR00208; GIADGLUTEN.
 DR PRINTS; PR00209; GIADIN.
 DR SMART; SM00499; AAI; 1.
 FT CHAIN 1 274 alpha-gliadin.
 SQ SEQUENCE 274 AA; 31980 MW; 97691937534ABD CRC64;

Query Match 84.5%; Score 82; DB 2; Length 274;
 Best Local Similarity 87.5%; Pred. No. 0.0063;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

DB 1 QLOPFPQPELPYPOQ 16
 58 QLOPFPQPELPYPOQ 73

RESULT 10

GD40 WHEAT STANDARD; PRT; 286 AA.

DR GD40 WHEAT
 AC P02863;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Alpha/beta-gliadin precursor (Prolamin).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Newton;
 RA MEDLINE=84267434; PubMed=6204862;
 RA Rafalski J.A., Scheets K., Metzler W., Peterson D.M., Hedgcock C.,
 RA Soli D.G.;
 RL "Developmentally regulated plant genes: the nucleotide sequence of a wheat gliadin genomic clone.";
 EMBO J. 3:1409-1415(1984).
 [2]
 RN SEQUENCE FROM N.A. (CLONE PM8233).
 RP MEDLINE=85242077; PubMed=3839304;
 RA Summer-Smith M., Rafalski J.A., Sugiyama T., Stoll M., Soell D.;
 RL "Conservation and variability of wheat alpha/beta-gliadin genes.";
 Nucleic Acids Res. 13:3905-3916(1985).
 [3]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=85062803; PubMed=6095191;
 RA Anderson O.D., Hlits J.C., Gautier M.F., Greene F.C.;
 RL "Nucleic acid sequence and chromosome assignment of a wheat storage protein gene.";
 Nucleic Acids Res. 12:8129-8144(1984).
 [4]
 RN FUNCTION: Gliadin is the major seed storage protein in wheat.
 [5]
 RN -!- PTM: Substrate of transglutaminase (By similarity).
 [6]
 RN -!- ALLERGEN: Causes an allergic reaction in human. Is the cause of the celiac disease, also known as celiac sprue or gluten-sensitive enteropathy (By similarity).
 [7]
 RN -!- MISCELLANEOUS: The alpha/beta-gliadins can be divided into 5 homology classes. Sequence divergence between the classes is due to single base substitutions and to duplications or deletions within or near direct repeats. There are more than a 100 copies of the gene for alpha/beta-gliadin per haploid genome.

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CC -----
 DR EMBL; X00627; CAA25261.1; -
 DR EMBL; K03076; AAA34280.1; -
 DR EMBL; X02539; CAA26384.1; -
 DR EMBL; X01130; CAA25593.1; -
 DR PIR; A03354; EEMTA
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gli_a_glutenin.
 DR Pfam; PF00234; Tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 KM Allergen; Multigene family; Repeat; Seed storage protein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 286 Alpha/beta-gliadin.
 FT VARIANT 37 37 L -> Q (in clone PM8233 and in Ref. 3).
 FT VARIANT 93 93 P -> Q (in clone PM8233).
 FT VARIANT 193 194 HN -> LK (in Ref. 3).
 SQ SEQUENCE 286 AA; 32949 MW; E5ECFABBE29E10C6 CRC64;

Query Match 84.5%; Score 82; DB 1; Length 286;
 Best Local Similarity 87.5%; Pred. No. 0.0067;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
 DB 77 QLOPFPQPLPYPOQ 92

RESULT 11

AAA96525 PRELIMINARY; PRT; 286 AA.

ID AAA96525 PRELIMINARY; PRT; 286 AA.
 AC AAA96525;
 DT 02-VAR-2004 (TREMBlrel. 27, Created)
 DT 02-VAR-2004 (TREMBlrel. 27, Last sequence update)
 DT 02-VAR-2004 (TREMBlrel. 27, Last annotation update)
 DE Alpha-gliadin storage protein.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cheyenne;
 RA Anderson O.D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U51307; AAA96525.1; -
 SQ SEQUENCE 286 AA; 32949 MW; E5ECFABBE29E10C6 CRC64;

Query Match 84.5%; Score 82; DB 2; Length 286;
 Best Local Similarity 87.5%; Pred. No. 0.0067;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
 DB 77 QLOPFPQPLPYPOQ 92

RESULT 12

Q41528 PRELIMINARY; PRT; 287 AA.

ID Q41528 PRELIMINARY; PRT; 287 AA.
 AC Q41528;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-VAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Alpha-gliadin
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.

OX NCBI_TaxID=4565;

RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=Cheyenne;
 RA Anderson O.D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50984; AAA96276.1; -
 DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gli_a_glutenin.
 DR Pfam; PF00234; Tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 SQ SEQUENCE 287 AA; 33193 MW; 05F8296749C9E97 CRC64;

Query Match 84.5%; Score 82; DB 2; Length 287;
 Best Local Similarity 87.5%; Pred. No. 0.0067;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
 DB 76 QLOPFPQPLPYPOQ 91

RESULT 13

Q9ZP09 PRELIMINARY; PRT; 288 AA.

ID Q9ZP09 PRELIMINARY; PRT; 288 AA.
 AC Q9ZP09;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Alpha-gliadin precursor (Fragment).
 GN Name=alpha-gliadin;
 OS Triticum aestivum subsp. spelta.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OX NCBI_TaxID=58933;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kaerstad D.D.; D'Ovidio R.;
 RT "Purified amino acid sequence of an alpha-gliadin gene from Spelt wheat (Spelta) includes sequences active in celiac disease.";
 RL Cereal Chem. 76:548-551 (1999).
 DR EMBL; AJ130948; CAA10257.1; -
 DR PIR; S13333; S13333.
 DR GO; GO:0045735; F.nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gli_a_glutenin.
 DR Pfam; PF00234; Tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.

Query Match 84.5%; Score 82; DB 2; Length 288;
 Best Local Similarity 87.5%; Pred. No. 0.0067;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
 DB 77 QLOPFPQPLPYPOQ 92

Query Match 84.5%; Score 82; DB 2; Length 288;
 Best Local Similarity 87.5%; Pred. No. 0.0067;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
 DB 77 QLOPFPQPLPYPOQ 92

RESULT 14

Q41531

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ID Q41531 PRELIMINARY; PRT; 289 AA.
AC Q41531;
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, last sequence update)
DT 01-MAR-2004 (TREMBLER. 26, last annotation update)
DE Alpha-gliadin storage protein.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OC NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RG STRAIN=Cheyenne;
RA Anderson O.D.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51306; AAA96524.1; -.
DR PIR; S13333; S13333.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001376; Gliadin.
DR InterPro; IPR001954; G1ia_glutenin.
DR Pfam; PF00234; TYP_alpha_amy1; 1.
DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAI; 1.
SQ SEQUENCE 289 AA; 33349 MM; 5F577C9CD63874FA CRC64;

Query Match 84.5%; Score 82; DB 2; Length 289;
Best Local Similarity 87.5%; Pred. No. 0.0067;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QLOFPPOPELPPYPOQ 16
|||
77 QLOFPPOPELPPYPOQ 92

RESULT 15
Q41545
ID Q41545 PRELIMINARY; PRT; 318 AA.
AC Q41545;
DT 01-NOV-1996 (TREMBLER. 01, Created)
DT 01-NOV-1996 (TREMBLER. 01, last sequence update)
DT 01-MAR-2004 (TREMBLER. 26, last annotation update)
DE (T. aestivum) alpha-type gliadin precursor.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OC NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84272703; PubMed=6589619;
RA Kasarda D.D., Okita T.W., Bernardin J.E., Baecker P.A., Nimmo C.C.,
RA Lew E.J.-L., Dietler W.D., Greene F.C.;
RT "Nucleic acid (cDNA) and amino acid sequences of alpha-type gliadins
RT from wheat (Triticum aestivum).";
RT Proc. Natl. Acad. Sci. U.S.A. 81:4712-4716(1984).
DR EMBL; K02068; AAA34275.1; -.
DR PIR; S13333; S13333.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001376; Gliadin.
DR InterPro; IPR001954; G1ia_glutenin.
DR Pfam; PF00234; TYP_alpha_amy1; 1.
DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAI; 1.
RN [1]
RP SIGNAL.
RT CHAIN 21 318 Potential.
SQ SEQUENCE 318 AA; 36538 MM; 758596B45DEC32D CRC64;

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Query Match 84.5%; Score 82; DB 2; Length 318;
 Best Local Similarity 76.2%; Pred. No. 0.0075;
 Matches 16; Conservative 1; Mismatches 0; Indels 4; Gaps 1;

OY 1 QLOFPPOPE----LPYPOQS 17
 |||
 DB 77 QLOFPPOPEPPLPYPOQS 97

Search completed: December 14, 2004, 17:06:09
 Job time : 179.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07 ; Search time 33.2917 Seconds
(without alignments)
49.132 Million cell updates/sec

Title: US-10-089-700-2
Perfect score: 97
Sequence: 1 QLQFPQPQLPYRPPQ 17

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	92.8	291	2	T06498
2	90	92.8	297	2	T06500
3	90	92.8	307	2	S10015
4	82	84.5	286	1	BEWTA
5	82	84.5	286	2	S07923
6	81.5	84.0	313	2	S07924
7	81.5	84.0	319	2	A22364
8	77.5	79.9	319	2	C22364
9	77.5	79.9	326	2	D22364
10	74	76.3	288	2	T06282
11	72.5	74.7	296	2	A27319
12	72.5	74.7	296	2	S07361
13	66.5	66.6	347	2	T05737
14	63.5	65.5	282	2	T06504
15	63.5	65.5	320	2	E22364
16	63	64.9	194	2	A23277
17	63	64.9	302	2	JA0153
18	62.5	64.4	292	2	B22364
19	62.5	64.4	357	2	S18235
20	62.5	64.4	357	2	S18235
21	61	62.9	162	2	T07173
22	60.5	62.4	72	2	A25677
23	60.5	62.4	260	2	S18350
24	60.5	62.4	310	2	T06211
25	60.5	62.4	400	2	S58222
26	59.5	61.3	228	2	JT0564
27	59.5	61.3	291	1	BEWTA
28	59.5	61.3	327	2	US0402
29	58.5	60.3	105	2	S07189

30	56.5	58.2	302	2	H96792
31	56.2	56.2	138	2	B27863
32	54.5	56.2	427	2	T03955
33	54.5	56.2	807	2	T02916
34	54.5	56.2	839	1	TQ2MCA
35	54	55.7	251	2	PS0094
36	54	55.7	305	2	S08312
37	53.5	55.2	290	2	S20519
38	53.5	55.2	633	1	S49611
39	53.5	55.2	1494	2	T14355
40	53	54.6	286	2	T05718
41	52.5	54.1	271	2	T04474
42	52.5	54.1	284	2	A35419
43	52.5	54.1	293	2	S07365
44	52.5	54.1	3164	1	WMBEH6
45	52	53.6	728	2	S43768

ALIGNMENTS

RESULT 1

T06498
alpha/beta-gliadin A-II precursor - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06498
R/Okita, T.W.; Cheebrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92841; M01D:85234522; PMID:2889281
A/Accession: T06498
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-291 <OKI>
A/Cross-references: UNIPROT: P04722; EMBL: M10092; NID: G170711; PIDN: AAA34282.1; PID: G170
C/Superfamily: gliadin
C/Keywords: seed; storage protein
F: 1-20/Domain: signal sequence #status predicted <Sig>
F: 21-291/Product: alpha/beta-gliadin A-II #status predicted <MAT>

Query Match Best Local Similarity 92.8%; Score 90; DB 2; Length 291;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLQFPQPQLPYRPPQ 16
Db 77 QLQFPQPQLPYRPPQ 92

RESULT 2

T06500
alpha/beta-gliadin A-IV precursor - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06500
R/Okita, T.W.; Cheebrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92841; M01D:85234522; PMID:2889281
A/Accession: T06500
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-297 <OKI>
A/Cross-references: UNIPROT: P04724; EMBL: M11075; NID: G170723; PIDN: AAA34282.1; PID: G170
C/Superfamily: gliadin
C/Keywords: seed; storage protein
F: 1-20/Domain: signal sequence #status predicted <Sig>
F: 21-297/Product: alpha/beta-gliadin A-IV #status predicted <MAT>

Query Match Best Local Similarity 92.8%; Score 90; DB 2; Length 297;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPOQ 16
|||||:|||||
DB 77 QLOPFPQPELPYPOQ 92

RESULT 3

S10015

alpha/beta-gliadin precursor (clone MM1) - wheat

A:Species: Triticum aestivum (common wheat)

C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C:Accession: S10015

R:Garcia-Maroto, F.; Marana, C.; Garcia-Olmedo, F.; Carbonero, P.

P:ant Mol. Biol. 14, 867-868, 1990

A:Title: Nucleotide sequence of a cDNA encoding an alpha/beta-type gliadin from hexaploid

A:Reference number: S10015; MUID:91346673; PMID:2102855

A:Accession: S10015

A:Molecule type: mRNA

A:Residues: 1-307 <GAP>

A:Cross-references: UNIPROT:P18573; EMBL:X17361; NID:g21672; PIDN:CAA55238.1; PID:g21673

C:Superfamily: gliadin

P:21-307/Product: alpha/beta-gliadin #status predicted <SIG>

Query Match 92.8%; Score 90; DB 2; Length 307;
Best Local Similarity 93.8%; Pred. No. 7.1e-05;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPOQ 16
|||||:|||||
DB 77 QLOPFPQPELPYPOQ 92

RESULT 4

EMBL

alpha/beta-gliadin precursor - wheat

A:Alternate names: prolamin

C:Species: Triticum aestivum (common wheat)

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03354

R:Rafalski, J.A.; Scheets, K.; Metzler, M.; Peterson, D.M.; Hedgcock, C.; Soll, D.G.

EMBL J. 3, 1409-1415, 1984

A:Title: Developmentally regulated plant genes: the nucleotide sequence of a wheat gliad

A:Reference number: A03354; MUID:84261434; PMID:6204862

A:Accession: A03354

A:Molecule type: DNA

A:Residues: 1-286 <RAP>

A:Cross-references: UNIPROT:P02863; GB:X00627; GB:X03076; NID:g21752; PIDN:CAA25261.1; F

A:Experimental source: cv. Newton

C:Comment: Gliadin is the major seed storage protein in wheat.

C:Superfamily: gliadin

C:Keywords: storage protein; tandem repeat

E:1-20/Domain: signal sequence #status predicted <SIG>

F:16-108/Region: 6-residue repeats (IQP)-Q-Q-P-[FY]-P

F:21-286/Product: gliadin #status predicted <GLN>

F:116-133/Region: glutamine-rich

Query Match 84.5%; Score 82; DB 1; Length 286;
Best Local Similarity 87.5%; Pred. No. 0.00076;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPOQ 16
|||||:|||||
DB 77 QLOPFPQPELPYPOQ 92

RESULT 5

S07923

alpha/beta-gliadin precursor - wheat

A:Species: Triticum aestivum (common wheat)

C:Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 20-Aug-1999

C:Accession: S07923

R:Summer-Smith, M.; Rafalski, J.A.; Sugiyama, T.; Stoll, M.; Soell, D.

Nucleic Acids Res. 13, 3905-3916, 1985
A:Title: Conservation and variability of wheat alpha/beta-gliadin genes.
A:Reference number: S07361; MUID:85242077; PMID:3839304
A:Accession: S07923
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <SUM>
A:Cross-references: EMBL:X02539; NID:g21760; PIDN:CAA26384.1; PID:g21761

C:Superfamily: gliadin

Query Match 84.5%; Score 82; DB 2; Length 286;
Best Local Similarity 87.5%; Pred. No. 0.00076;
Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPELPYPOQ 16
|||||:|||||
DB 77 QLOPFPQPELPYPOQ 92

RESULT 6

S07924

alpha/beta-gliadin precursor - wheat

A:Species: Triticum aestivum (common wheat)

C:Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004

C:Accession: S07924; C61218

R:Summer-Smith, M.; Rafalski, J.A.; Sugiyama, T.; Stoll, M.; Soell, D.

Nucleic Acids Res. 13, 3905-3916, 1985

A:Title: Conservation and variability of wheat alpha/beta-gliadin genes.

A:Reference number: S07361; MUID:85242077; PMID:3839304

A:Accession: S07924

A:Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-313 <SUM>

A:Cross-references: UNIPROT:Q41546; EMBL:X02540; NID:g21764; PIDN:CAA26385.1; PID:g21765

R:Shewry, P.R.; Sabelli, P.A.; Panmar, S.; Lafandra, D.

Biochem. Genet. 29, 207-211, 1991

A:Title: alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynal

A:Reference number: A61218; MUID:91315394; PMID:1859356

A:Accession: C61218

A:Status: preliminary

A:Molecule type: protein

A:Residues: 18-27 <SHR>

C:Superfamily: gliadin

C:Keywords: seed; storage protein

Query Match 84.0%; Score 81.5; DB 2; Length 313;
Best Local Similarity 72.7%; Pred. No. 0.00097;
Matches 16; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOPFPQ-----PELPYPOQS 17
|||||:|||||
DB 74 QLOPFPQPELPYPOQ 95

RESULT 7

A22364

alpha/beta-gliadin precursor (clone A42) - wheat

A:Alternate names: prolamin

C:Species: Triticum aestivum (common wheat)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C:Accession: A22364

R:Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A:Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA

A:Reference number: A92541; MUID:85234522; PMID:2989281

A:Accession: A22364

A:Molecule type: mRNA

A:Residues: 1-319 <OKT>

A:Cross-references: UNIPROT:P04725; GB:M1073; NID:g170715; PIDN:AAA34278.1; PID:g17072

C:Superfamily: gliadin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-319/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 84.0%; Score 81.5; DB 2; Length 319;
 Best Local Similarity 72.7%; Pred. No. 0.00099;
 Matches 16; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOFPPO-----PELPYPOQ 17
 ||||| |
 Db 77 QLOFPPOQPPFPQPLPYPOQ 98

RESULT 8

D22364
 alpha/beta-gliadin precursor (clone A212) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: C22364
 R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
 J. Biol. Chem. 260, 8203-8213, 1985
 A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
 A/Reference number: A92541; MUID:85234522; PMID:2989281
 A/Accession: C22364
 A/Molecule type: mRNA
 A/Residues: 1-319 <OKT>
 A/Cross-references: UNIPROT:P04722
 C/Superfamily: gliadin
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-319/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 79.9%; Score 77.5; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 0.0033;
 Matches 15; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOFPPO-----PELPYPOQ 16
 ||||| |
 Db 77 QLOFPPOQPPFPQPLPYPOQ 97

RESULT 9

D22364
 alpha/beta-gliadin precursor (clone A735) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: D22364
 R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
 J. Biol. Chem. 260, 8203-8213, 1985
 A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
 A/Reference number: A92541; MUID:85234522; PMID:2989281
 A/Accession: D22364
 A/Molecule type: mRNA
 A/Residues: 1-326 <OKT>
 A/Cross-references: UNIPROT:P04724
 C/Superfamily: gliadin
 F/1-20/Domain: signal sequence #status predicted <SIG>
 F/21-326/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 79.9%; Score 77.5; DB 2; Length 326;
 Best Local Similarity 71.4%; Pred. No. 0.0034;
 Matches 15; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOFPPO-----PELPYPOQ 16
 ||||| |
 Db 77 QLOFPPOQPPFPQPLPYPOQ 97

RESULT 10

T06282
 alpha-gliadin precursor - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T06282
 R/Anderson, O.D.
 submitted to the EMBL Data Library, March 1996
 A/Reference number: Z15587
 A/Accession: T06282

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-288 <AND>
 A/Cross-references: UNIPROT:Q41530; EMBL:U51304; NID:g1256787; PIDD:AAA96523.1; PID:g12;
 A/Experimental source: cv. Cheyenne
 C/Superfamily: gliadin
 C/Keywords: seed; storage protein

Query Match 76.3%; Score 74; DB 2; Length 288;
 Best Local Similarity 81.2%; Pred. No. 0.0087;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QLOFPPOPELPYPOQ 16
 ||||| |
 Db 77 QLOFPPOQPPFPQPLPYPOQ 92

RESULT 11

A27319
 gliadin - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 04-Mar-1988 #sequence_revision 04-Mar-1988 #text_change 03-Feb-1994
 C/Accession: A27319
 R/Reeves, C.D.; Okita, T.W.
 Gene 52, 257-266, 1987
 A/Title: Analyses of alpha/beta-type gliadin genes from diploid and hexaploid wheats.
 A/Reference number: A27319; MUID:8727398; PMID:3036689
 A/Accession: A27319
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-296 <REE>
 C/Superfamily: gliadin

Query Match 74.7%; Score 72.5; DB 2; Length 296;
 Best Local Similarity 70.0%; Pred. No. 0.014;
 Matches 14; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOFPPO-----PELPYPOQ 15
 ||||| |
 Db 77 QLOFPPOQPPFPQPLPYPOQ 96

RESULT 12

S07361
 alpha/beta-gliadin precursor (clone PM215) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C/Accession: S07361
 R/Summer-Smith, M.; Rafalaki, J.A.; Sugiyama, T.; Stoll, M.; Seel, D.
 Nucleic Acids Res. 13, 3905-3916, 1985
 A/Title: Conservation and variability of wheat alpha/beta-gliadin genes.
 A/Reference number: S07361; MUID:85242077; PMID:3839304
 A/Accession: S07361
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-296 <SUM>
 A/Cross-references: UNIPROT:P04726; EMBL:X02538; NID:g21756; PIDD:CAA26383.1; PID:g2175
 C/Superfamily: gliadin
 C/Keywords: seed; storage protein

Query Match 74.7%; Score 72.5; DB 2; Length 296;
 Best Local Similarity 70.0%; Pred. No. 0.014;
 Matches 14; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOFPPO-----PELPYPOQ 15
 ||||| |
 Db 77 QLOFPPOQPPFPQPLPYPOQ 96

RESULT 13

T05737
 probable hordein C - barley
 C/Species: Hordeum vulgare (barley)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07 ; Search time 38.25 seconds
(without alignments)
29.475 Million cell updates/sec

Title: US-10-089-700-2

Perfect score: 97
Sequence: 1 QLOPPQPELPPQPOS 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	58.5	60.3	261 4	US-09-602-565-34 Sequence 34, Appl
2	53.5	55.2	613 4	US-09-345-473E-39 Sequence 39, Appl
3	52	53.6	728 4	US-09-508-824-10 Sequence 10, Appl
4	51.5	53.1	558 4	US-09-252-991A-17202 Sequence 17202, A
5	51	51.6	23 3	US-08-460-269C-8 Sequence 8, Appl
6	51	52.6	24 3	US-08-750-624-11 Sequence 11, Appl
7	51	52.6	24 4	US-08-261-194-11 Sequence 11, Appl
8	51	52.6	910 3	US-08-460-269C-2 Sequence 2, Appl
9	50	51.5	129 3	US-09-199-637A-57 Sequence 97, Appl
10	50	51.5	132 3	US-08-529-055-63 Sequence 63, Appl
11	50	51.5	204 4	US-09-248-796A-18436 Sequence 18, Appl
12	50	51.5	406 4	US-09-286-981B-18 Sequence 32, Appl
13	50	51.5	8991 4	US-08-714-741-33 Sequence 22774, A
14	49.5	51.0	81 4	US-09-248-796A-22774 Sequence 2, Appl
15	49	50.5	337 4	US-08-930-830B-2 Sequence 5, Appl
16	49	50.5	342 4	US-08-930-830B-5 Sequence 1371, Ap
17	49	50.5	2004 4	US-09-538-092-1371 Sequence 11, Appl
18	48	49.5	33 1	US-08-237-716-11 Sequence 22728, A
19	48	49.5	271 4	US-09-248-796A-22728 Sequence 1251, Ap
20	48	49.5	507 4	US-09-538-092-1251 Sequence 8, Appl
21	48	49.5	507 5	PCT-US93-08356-8 Sequence 45954, A
22	48	49.5	790 4	US-09-270-767-45954 Sequence 5, Appl
23	47.5	49.0	24 4	US-09-379-297-5 Sequence 79, Appl
24	47.5	49.0	24 4	US-09-703-399A-79 Sequence 38, Appl
25	47.5	49.0	35 1	US-08-471-780C-38 Sequence 38, Appl
26	47.5	49.0	35 1	US-08-467-282B-38 Sequence 38, Appl
27	47.5	49.0	35 2	US-08-471-282A-38 Sequence 38, Appl

28	47.5	49.0	35 2	US-08-466-710C-38 Sequence 38, Appl
29	47.5	49.0	35 3	US-08-468-739C-38 Sequence 38, Appl
30	47.5	49.0	35 4	US-09-293-769A-38 Sequence 44, Appl
31	47.5	49.0	54 1	US-08-471-780C-44 Sequence 44, Appl
32	47.5	49.0	54 1	US-08-467-282B-44 Sequence 44, Appl
33	47.5	49.0	54 2	US-08-467-282B-44 Sequence 44, Appl
34	47.5	49.0	54 2	US-08-466-710C-44 Sequence 44, Appl
35	47.5	49.0	54 3	US-08-468-739C-44 Sequence 44, Appl
36	47.5	49.0	54 4	US-09-293-769A-44 Sequence 87, Appl
37	47.5	49.0	60 1	US-08-471-780C-87 Sequence 87, Appl
38	47.5	49.0	60 1	US-08-467-282B-87 Sequence 87, Appl
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40	47.5	49.0	60 3	US-08-468-739C-87 Sequence 87, Appl
41	47.5	49.0	60 4	US-09-124-671-17 Sequence 25, Appl
42	47.5	49.0	60 3	US-09-124-671-17 Sequence 17, Appl
43	47.5	49.0	105 3	US-09-124-671-19 Sequence 19, Appl
44	47.5	49.0	109 3	US-09-124-671-19 Sequence 19, Appl
45	47.5	49.0	109 3	US-09-124-671-19 Sequence 19, Appl

ALIGNMENTS

```
RESULT 1
US-09-602-565-34
; Sequence 34, Application US/09602565
; Patent No. 6500642
; GENERAL INFORMATION:
; APPLICANT: Yue, Henry
; APPLICANT: Patterson, Chandra
; APPLICANT: Corley, Neil C.
; APPLICANT: Giesler, Karl J.
; TITLE OF INVENTION: MOLECULE ASSOCIATED WITH APOPTOSIS
; FILE REFERENCE: PC-0018 US
; CURRENT APPLICATION NUMBER: US/09/602,565
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/106,120
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PERL Program
; SEQ ID NO 34
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6500642 g1469400
US-09-602-565-34
Query Match 60.3%; Score 58.5; DB 4; Length 261;
Best Local Similarity 64.7%; Pred. No. 1.6;
Matches 11; Conservative 3; Mismatches 2; Indels 1; Gaps 1;
OY 1 QLOPPQPELPPQPO 16
Db 162 QLOPPQPELPPQPO 178
RESULT 2
US-09-345-473E-39
; Sequence 39, Application US/09345473E
; Patent No. 6558903
; GENERAL INFORMATION:
; APPLICANT: Hodge, Martin
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof
; FILE REFERENCE: 35800/183781
; CURRENT APPLICATION NUMBER: US/09/345,473E
; CURRENT FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 613
; TYPE: PRT
```


MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
FILING DATE: 26-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-660
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-750-624-11

Query Match 52.6%; Score 51; DB 3; Length 24;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 4 PFPQPELPYPOP 15
DB 11 PQQPEAPAPQP 22

RESULT 7
US-08-261-194-11:
Sequence 11, Application US/08261194
Patent No. 6764682
GENERAL INFORMATION:
APPLICANT: KANDIL, Ali
APPLICANT: JAMES, Olive A.
APPLICANT: KLEIN, Michel H.
APPLICANT: CHONG, Pele
TITLE OF INVENTION: ADJUVANT COMPOSITIONS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5T 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,194
FILING DATE: June 16, 1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-339 MIS-JB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-261-194-11

Query Match 52.6%; Score 51; DB 4; Length 24;
Best Local Similarity 75.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 4 PFPQPELPYPOP 15
DB 11 PQQPEAPAPQP 22

RESULT 8
US-08-460-269C-2
Sequence 2, Application US/08460269C
Patent No. 6197548
GENERAL INFORMATION:
APPLICANT: CLARE, JEFFREY J.
ROMANOS, MICHAEL A.
TITLE OF INVENTION: EXPRESSION OF HETEROLOGOUS PROTEIN IN YEAST
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Millen, White, Zelano & Branigan, P.C.
STREET: 2200 Clarendon Blvd., Suite 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,269C
FILING DATE: 02-Jun-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lebovitz, Richard M.
REGISTRATION NUMBER: 37,067
REFERENCE/DOCKET NUMBER: Popov-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 243-6333
TELEFAX: (703) 243-6410
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 910 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-08-460-269C-2

Query Match 52.6%; Score 51; DB 3; Length 910;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 4 PFPQPELPYPOP 15
DB 589 PQQPEAPAPQP 600

RESULT 9
US-09-199-637A-97
Sequence 97, Application US/09199637A
Patent No. 6355411
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
APPLICANT: Mahajan-Miklos, Shalina
APPLICANT: Tan, Man-Wah
APPLICANT: Cao, Hui
APPLICANT: Drenkard, Eliana
APPLICANT: Tsongalis, John

TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR APPLICATION NUMBER: 60/066,517
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 97
LENGTH: 129
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-97

Query Match 51.5%; Score 50; DB 3; Length 129;
Best Local Similarity 64.3%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 QPPEPPELPYPOQ 16
DB 16 RPPPEPRLPPRPPO 29

RESULT 10
US-08-529-055-63
Sequence 63, Application US/08529055
Patent No. 6592876

GENERAL INFORMATION:
APPLICANT: Briles, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swiatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Brooks-Walter, Alexis
TITLE OF INVENTION: Pneumococcal Genes, Portions
TITLE OF INVENTION: Thereof, Expression Products
TITLE OF INVENTION: Therefrom, and Uses of Such Genes,
TITLE OF INVENTION: Portions and Products
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,055
FILING DATE: 15-SEP-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2400
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-529-055-63

Query Match 51.5%; Score 50; DB 4; Length 132;
Best Local Similarity 64.3%; Pred. No. 10;

Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 4 PPEPPELPYPOQS 17
DB 119 PAPPEEQPAPAPKS 132

RESULT 11
US-09-248-796A-18436
Sequence 18436, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107136.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18436
LENGTH: 204
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-18436

Query Match 51.5%; Score 50; DB 4; Length 204;
Best Local Similarity 62.5%; Pred. No. 16;
Matches 10; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 QLOPPEPPELPYPOQ 16
DB 92 QQQQQPPAPQPPQPPQ 107

RESULT 12
US-09-286-981B-18
Sequence 18, Application US/09286981B
Patent No. 6503511
GENERAL INFORMATION:
APPLICANT: Witzmann, Theresa M.
APPLICANT: Koenig, Scott
APPLICANT: Johnson, Leslie S
TITLE OF INVENTION: Derivatives of Choline Binding Proteins for Vaccines
FILE REFERENCE: 469201-396
CURRENT APPLICATION NUMBER: US/09/286,981B
CURRENT FILING DATE: 1999-04-06
PRIOR APPLICATION NUMBER: US 60/085,743
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 406
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-286-981B-18

Query Match 51.5%; Score 50; DB 4; Length 406;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 PPEPPELPYPOQS 17
DB 378 PAPPEEQPAPAPKPN 391

RESULT 13
US-08-714-741-32
Sequence 32, Application US/08714741
Patent No. 6500613


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GENERAL INFORMATION:
APPLICANT: Bries, David E.
APPLICANT: McDaniel, Larry S.
APPLICANT: Swatlo, Edwin
APPLICANT: Yother, Janet
APPLICANT: Crain, Marilyn J.
APPLICANT: Hollingshead, Susan
APPLICANT: Tart, Rebecca
APPLICANT: Brooks-Walker, Alexis
TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
TITLE OF INVENTION: PORTIONS AND PRODUCTS
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.
ZIP: 10036
COMPUTER AVAILABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,741
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Frommer Esq., William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454312-2460
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 8991 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-08-714-741-32

Query Match 51.5%; Score 50; DB 4; Length 8991;
Best Local Similarity 64.3%; Pred. No. 7.1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

CY 4 PFPQPELPYPOPOS 17
DB 7523 PAPQPEOPAPAPKS 7536

RESULT 14
US-09-248-796A-22774
Sequence 22774, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANT
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 22774
LENGTH: 91
TYPE: PRT

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: ORGANISM: Candida albicans
US-09-248-796A-22774

Query Match          51.0%; Score 49.5; DB 4; Length 81;
Best Local Similarity 52.9%; Pred. No. 7.4;
Matches 9; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

OY      1  QLOPFPOPELPPPOPOS 17
      :|:|:|:|:|:|:|:|:|
Db      53 ELEPEPEPE-PEPEPES 68

RESULT 15
US-08-930-830B-2
: Sequence 2, Application US/08930830B
: Patent No. 6514712
: GENERAL INFORMATION:
: APPLICANT: Peters, Heiko
: APPLICANT: Bailing, Rudolf
: APPLICANT: Hoeller, Heinz
: APPLICANT: Richer, Thomas
: TITLE OF INVENTION: No. 6514712el probe for early diagnosis of epithelial
: TITLE OF INVENTION: dysplasias of the stratified squamous epithelium and for
: TITLE OF INVENTION: tumour diagnosis and tumour therapy of squamous epithelial
: TITLE OF INVENTION: carcinomas
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NIXON & VANDERHAYE P.C.
: STREET: 1100 No. 6514712th Glebe Rd. 8th floor
: CITY: Arlington
: STATE: VA
: COUNTRY: USA
: ZIP: 22201-4741
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/930, 830B
: FILING DATE: 16-JAN-1998
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/EP97/00564
: FILING DATE: 07-FEB-1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: GB 19605105.3
: FILING DATE: 12-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Sadboff, B.J.
: REGISTRATION NUMBER: 36, 663
: REFERENCE/DOCKET NUMBER: 2861-6
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 703-816-4000
: TELEFAX: 703-816-4100
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 337 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-930-830B-2

Query Match          50.5%; Score 49; DB 4; Length 337;
Best Local Similarity 52.4%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 4; Indels 6; Gaps 1;

OY      1  QLOPPPOPELP-----YPOP 15
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Db      143 QHQPFPQPALPYNHIVSYSPSP 163

Search completed: December 14, 2004, 17:00:57
Job time : 39.25 secs

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 14, 2004, 16:56:07 ; Search time 141.667 Seconds
(without alignments)
42.861 Million cell updates/sec

Title: US-10-089-700-2

Perfect score: 97

Sequence: 1 QLOPFPQELPFPQPS 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/1/pubpaa/PCTI_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	92.8	33	US-10-367-405-12	Sequence 12, Appl
2	90	92.8	298	US-10-733-930-5770	Sequence 9777, Ap
3	82	84.0	287	US-10-733-930-5777	Sequence 9777, Ap
4	81.5	84.5	319	US-10-733-930-5619	Sequence 9619, Ap
5	69	71.1	12	US-10-367-405-14	Sequence 14, Appl
6	66	68.0	12	US-10-367-405-1	Sequence 1, Appl
7	66	68.0	12	US-10-367-405-2	Sequence 2, Appl
8	66	68.0	12	US-10-474-955-15	Sequence 15, Appl
9	66	68.0	13	US-10-367-405-17	Sequence 17, Appl
10	66	68.0	14	US-10-367-405-18	Sequence 18, Appl
11	63.5	65.5	34	US-10-367-405-24	Sequence 24, Appl
12	63	64.9	13	US-10-367-405-4	Sequence 4, Appl
13	63	64.9	14	US-10-367-405-3	Sequence 3, Appl

ALIGNMENTS

14	63	64.9	14	US-10-367-405-15	Sequence 15, Appl
15	63	64.9	14	US-10-474-955-14	Sequence 14, Appl
16	63	64.9	20	US-10-474-955-25	Sequence 25, Appl
17	63	64.9	17	US-10-474-955-101	Sequence 101, Appl
18	63	64.9	282	US-10-474-955-101	Sequence 101, Appl
19	62.5	64.4	19	US-10-239-313A-409	Sequence 409, Appl
20	62.5	64.4	21	US-10-474-955-52	Sequence 52, Appl
21	60.5	62.4	14	US-10-367-405-7	Sequence 7, Appl
22	60.5	62.4	400	US-10-301-822-135	Sequence 135, Appl
23	60.5	62.4	400	US-10-367-405-17	Sequence 17, Appl
24	59.5	61.3	883	US-10-437-920-9623	Sequence 9623, Appl
25	59.5	61.3	327	US-10-739-920-9623	Sequence 9623, Appl
26	58.5	60.8	11	US-10-367-405-5	Sequence 5, Appl
27	58.5	60.8	327	US-10-367-405-5	Sequence 5, Appl
28	58.5	60.8	14	US-10-280-953-17	Sequence 17, Appl
29	58.5	60.8	261	US-09-855-754-21	Sequence 21, Appl
30	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
31	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
32	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
33	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
34	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
35	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
36	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
37	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
38	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
39	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
40	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
41	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
42	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
43	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
44	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl
45	58.5	60.8	52	US-10-302-896-21	Sequence 21, Appl

RESULT 1
US-10-367-405-12
Sequence 12, Application US/10367405
Publication No. US20030215438A1
GENERAL INFORMATION:
APPLICANT: Felix Hauech
APPLICANT: Gary Gray
APPLICANT: Chaitan Khosla
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
FILE REFERENCE: STAN-258US1
CURRENT APPLICATION NUMBER: US/10/367,405
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/357,238
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/380,761
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/392,782
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/422,933
PRIOR FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: 60/428,033
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: 60/435,881
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 33
TYPE: PRT
ORGANISM: triticum aestivum

Query Match 92.8% Score 90; DB 14; Length 33;
Best Local Similarity 93.8%; Pred. NO. 0.00049;
Matches 15; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
DB 2 QLOPFPQPLPYPOQ 17

RESULT 2

US-10-739-930-9770

Sequence 9770, Application US/10739930
Publication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 9770

LENGTH: 298

TYPE: PRT

ORGANISM: Triticum aestivum

OTHER INFORMATION: Clone ID: TRIA-23APR03-C176_183.p

Query Match

Best Local Similarity 92.8%; Score 90; DB 17; Length 298;

Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
DB 77 QLOPFPQPLPYPOQ 92

RESULT 3

US-10-739-930-9777

Sequence 9777, Application US/10739930
Publication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 9777

LENGTH: 287

TYPE: PRT

ORGANISM: Triticum aestivum

OTHER INFORMATION: Clone ID: TRIA-23APR03-C176_238.p

Query Match

Best Local Similarity 84.5%; Score 82; DB 17; Length 287;

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPYPOQ 16
DB 77 QLOPFPQPLPYPOQ 92

RESULT 4

US-10-739-930-9619

Sequence 9619, Application US/10739930
Publication No. US20040216190A1

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-21(53377)B

;; CURRENT APPLICATION NUMBER: US/10/739,930
;; CURRENT FILING DATE: 2003-12-18
;; NUMBER OF SEQ ID NOS: 11088
;; SEQ ID NO 9619
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Triticum aestivum
;; FEATURE:
;; OTHER INFORMATION: Clone ID: TRIA-23APR03-C125_59.p
US-10-739-930-9619

Query Match 84.0%; Score 81.5; DB 17; Length 319;
Best Local Similarity 72.7%; Pred. No. 0.043;
Matches 16; Conservative 1; Mismatches 0; Indels 5; Gaps 1;

QY 1 QLOPFPQPLPYPOQ 17
DB 77 QLOPFPQPLPYPOQ 98

RESULT 5

US-10-367-405-14

Sequence 14, Application US/10367405
Publication No. US20030215438A1

GENERAL INFORMATION:

APPLICANT: Felix Hausch

APPLICANT: Gary Gray

APPLICANT: Lu Shan

TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE

FILE REFERENCE: STAN-2580S1

CURRENT APPLICATION NUMBER: US/10/367,405

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/357,238

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: 60/380,761

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/392,782

PRIOR FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: 60/422,933

PRIOR FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: 60/428,033

PRIOR FILING DATE: 2002-11-20

PRIOR APPLICATION NUMBER: 60/435,881

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 14

LENGTH: 12

TYPE: PRT

ORGANISM: Triticum aestivum

US-10-367-405-14

Query Match 71.1%; Score 69; DB 14; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QLOPFPQPLPY 12
DB 1 QLOPFPQPLPY 12

RESULT 6

US-10-367-405-1

Sequence 1, Application US/10367405
Publication No. US20030215438A1

GENERAL INFORMATION:

APPLICANT: Felix Hausch

APPLICANT: Gary Gray

APPLICANT: Lu Shan

APPLICANT: Chaitan Khosla

TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE

FILE REFERENCE: STAN-2580S1

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/ CURRENT APPLICATION NUMBER: US/10/367,405
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/357,238
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: 60/380,761
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 60/392,782
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/428,033
/ PRIOR FILING DATE: 2002-11-20
/ PRIOR APPLICATION NUMBER: 60/435,881
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 1
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-367-405-1
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Query Match      68.0%; Score 66; DB 14; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 QLOPFPQPLPY 12
Db 1 QLOPFPQPLPY 12
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RESULT 7
US-10-367-405-2
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/ Sequence 2, Application US/10367405
/ Publication No. US20030215438A1
/ GENERAL INFORMATION:
/ APPLICANT: Felix Hausch
/ APPLICANT: Gary Gray
/ APPLICANT: Lu Shan
/ APPLICANT: Chaitan Khosla
/ TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
/ FILE REFERENCE: STAN-258US1
/ CURRENT APPLICATION NUMBER: US/10/367,405
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/357,238
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: 60/380,761
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 60/392,782
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/428,033
/ PRIOR FILING DATE: 2002-11-20
/ PRIOR APPLICATION NUMBER: 60/435,881
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 2
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
/ NAME/KEY: PYRROLIDONE CAR
/ LOCATION: (1)...(1)
/ OTHER INFORMATION: N terminal pyroglutamate
US-10-367-405-2
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Query Match      68.0%; Score 66; DB 14; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 QLOPFPQPLPY 12
```

```
Db 1 QLOPFPQPLPY 12
```

```
RESULT 8
US-10-474-955-15
/ Sequence 15, Application US/10474955
/ Publication No. US20040241161A1
/ GENERAL INFORMATION:
/ APPLICANT: Drijfhout, Jan W.
/ APPLICANT: Konings, Frits
/ APPLICANT: McAdam, Stephen N.
/ APPLICANT: Ludwig, Solliid Magne
/ TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
/ FILE REFERENCE: 2799/71244-PCT-US
/ CURRENT APPLICATION NUMBER: US/10/474,955
/ CURRENT FILING DATE: 2003-10-13
/ NUMBER OF SEQ ID NOS: 137
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 15
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Epitope G1a-ALPHA9 (57-68)
US-10-474-955-15
```

```
Query Match      68.0%; Score 66; DB 17; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.13;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 QLOPFPQPLPY 12
Db 1 QLOPFPQPLPY 12
```

```
RESULT 9
US-10-367-405-17
/ Sequence 17, Application US/10367405
/ Publication No. US20030215438A1
/ GENERAL INFORMATION:
/ APPLICANT: Felix Hausch
/ APPLICANT: Gary Gray
/ APPLICANT: Lu Shan
/ APPLICANT: Chaitan Khosla
/ TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
/ FILE REFERENCE: STAN-258US1
/ CURRENT APPLICATION NUMBER: US/10/367,405
/ CURRENT FILING DATE: 2003-02-14
/ PRIOR APPLICATION NUMBER: 60/357,238
/ PRIOR FILING DATE: 2002-02-14
/ PRIOR APPLICATION NUMBER: 60/380,761
/ PRIOR FILING DATE: 2002-05-14
/ PRIOR APPLICATION NUMBER: 60/392,782
/ PRIOR FILING DATE: 2002-06-28
/ PRIOR APPLICATION NUMBER: 60/422,933
/ PRIOR FILING DATE: 2002-10-31
/ PRIOR APPLICATION NUMBER: 60/428,033
/ PRIOR FILING DATE: 2002-11-20
/ PRIOR APPLICATION NUMBER: 60/435,881
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 17
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Triticum aestivum
US-10-367-405-17
```

```
Query Match      68.0%; Score 66; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 6 POPELPPPOQ 16
 |||||
 Db 1 POPELPPPOQ 11

RESULT 10

US-10-367-405-18

Sequence 18, Application US/10367405
 Publication No. US20030215438A1

GENERAL INFORMATION:

APPLICANT: Felix Hausch

APPLICANT: Gary Gray

APPLICANT: Lu Shan

APPLICANT: Chaitan Khosla

TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE

FILE REFERENCE: STAN-258US1

CURRENT APPLICATION NUMBER: US/10/367,405

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/357,238

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: 60/380,761

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/392,782

PRIOR FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: 60/422,933

PRIOR FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: 60/428,033

PRIOR FILING DATE: 2002-11-20

PRIOR APPLICATION NUMBER: 60/435,881

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 18

LENGTH: 14

TYPE: PRT

ORGANISM: Triticum aestivum

US-10-367-405-18

Query Match 68.0%; Score 66; DB 14; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 POPELPPPOQ 16

|||||

Db 1 POPELPPPOQ 11

RESULT 11

US-10-367-405-24

Sequence 24, Application US/10367405
 Publication No. US20030215438A1

GENERAL INFORMATION:

APPLICANT: Felix Hausch

APPLICANT: Gary Gray

APPLICANT: Lu Shan

APPLICANT: Chaitan Khosla

TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE

FILE REFERENCE: STAN-258US1

CURRENT APPLICATION NUMBER: US/10/367,405

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/357,238

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: 60/380,761

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/392,782

PRIOR FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: 60/422,933

PRIOR FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: 60/428,033

PRIOR FILING DATE: 2002-11-20

PRIOR APPLICATION NUMBER: 60/435,881

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 27
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 24
 LENGTH: 34
 TYPE: PRT
 ORGANISM: Triticum aestivum

US-10-367-405-24

Query Match 65.5%; Score 63.5; DB 14; Length 34;
 Best Local Similarity 75.0%; Pred. No. 0.71;
 Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 QLOPPPOPELPPPOQ 16

|||||

Db 13 QLOPPPOPELPPPOQ 27

RESULT 12

US-10-367-405-4

Sequence 4, Application US/10367405
 Publication No. US20030215438A1

GENERAL INFORMATION:

APPLICANT: Felix Hausch

APPLICANT: Gary Gray

APPLICANT: Lu Shan

APPLICANT: Chaitan Khosla

TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE

FILE REFERENCE: STAN-258US1

CURRENT APPLICATION NUMBER: US/10/367,405

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/357,238

PRIOR FILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: 60/380,761

PRIOR FILING DATE: 2002-05-14

PRIOR APPLICATION NUMBER: 60/392,782

PRIOR FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: 60/422,933

PRIOR FILING DATE: 2002-10-31

PRIOR APPLICATION NUMBER: 60/428,033

PRIOR FILING DATE: 2002-11-20

PRIOR APPLICATION NUMBER: 60/435,881

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 4

LENGTH: 13

TYPE: PRT

ORGANISM: Triticum aestivum

US-10-367-405-4

Query Match 64.9%; Score 63; DB 14; Length 13;
 Best Local Similarity 90.9%; Pred. No. 0.33;
 Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 POPELPPPOQ 16

|||||

Db 1 POPELPPPOQ 11

RESULT 13

US-10-367-405-3

Sequence 3, Application US/10367405
 Publication No. US20030215438A1

GENERAL INFORMATION:

APPLICANT: Felix Hausch

APPLICANT: Gary Gray

APPLICANT: Lu Shan

APPLICANT: Chaitan Khosla

TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE

FILE REFERENCE: STAN-258US1

CURRENT APPLICATION NUMBER: US/10/367,405

CURRENT FILING DATE: 2003-02-14

PRIOR APPLICATION NUMBER: 60/357,238

```
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-3
```

```
Query Match          64.9%; Score 63; DB 14; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.35;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 PGPPLPYPOPO 16
      |||:|||||
Db      1 PGPPLPYPOPO 11
```

```
RESULT 14
US-10-367-405-15
; Sequence 15, Application US/10367405
; Publication No. US20030215438A1
; GENERAL INFORMATION:
; APPLICANT: Felix Hausch
; APPLICANT: Gary Gray
; APPLICANT: Lu Shan
; APPLICANT: Chaitan Khosla
; TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR CELIAC SPRUE
; FILE REFERENCE: STAN-258US1
; CURRENT APPLICATION NUMBER: US/10/367,405
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/357,238
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: 60/380,761
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/392,782
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/422,933
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: 60/428,033
; PRIOR FILING DATE: 2002-11-20
; PRIOR APPLICATION NUMBER: 60/435,881
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 15
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-367-405-15
```

```
Query Match          64.9%; Score 63; DB 14; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.35;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 PGPPLPYPOPO 16
      |||:|||||
Db      1 PGPPLPYPOPO 11
```

```
RESULT 15
US-10-474-955-14
; Sequence 14, Application US/10474955
```

```
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Diffhout, Jan W.
; APPLICANT: Koning, Frits
; APPLICANT: McAdam, Stephen N.
; APPLICANT: Ludwig, Soiliid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; PRIOR FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitope Gila-ALPHA2 (62-75)
US-10-474-955-14
```

```
Query Match          64.9%; Score 63; DB 17; Length 14;
Best Local Similarity 90.9%; Pred. No. 0.35;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 PGPPLPYPOPO 16
      |||:|||||
Db      1 PGPPLPYPOPO 11
```

```
Search completed: December 14, 2004, 17:09:34
Job time : 141.667 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2004, 17:00:05 ; Search time 76.6667 Seconds
(without alignments)
1244.635 Million cell updates/sec

Title: US-10-089-700-3-H65

Perfect score: 1434

Sequence: 1 VRVVPQLQPNPQSQPOE.....CNVIAPYCTIAPFGIGTN 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1426	99.4	266	AAU01799	Wheat A-G
2	1426	99.4	266	ADH14513	A-glutinin
3	1266.5	88.3	290	AAE38574	Wheat alp
4	1266.5	88.3	290	ADP19626	Alpina-2-G
5	463	32.3	369	AAW62647	Mature du
6	450.5	31.6	297	AD071659	Amino aci
7	439.5	30.6	307	ADH89338	T. aestiv
8	439.5	30.6	307	ADH89338	T. aestiv
9	437.5	30.5	298	AD071661	Amino aci
10	290.5	20.3	1798	ABB71695	Drosophil
11	271	18.9	2285	ABB63057	Drosophil
12	268	18.7	1162	AAV96255	Kaposi's
13	268	18.7	1162	AAV96255	Kaposi's
14	268	18.7	1162	AAV96255	Kaposi's
15	268	18.7	1162	AAV96255	Kaposi's
16	268	18.7	1162	AAV96255	Kaposi's
17	265.5	18.5	1069	ABO07138	Human pol
18	265.5	18.5	1069	ABO07138	Human pol
19	265.5	18.5	1069	ABO07138	Human pol
20	259	18.1	905	ABG93053	S. cerevi
21	259	18.1	905	ABG93053	S. cerevi
22	259	18.1	905	ABG93053	S. cerevi
23	254	17.7	186	ADH89336	H. vulgar
24	254	17.7	186	ADH89336	H. vulgar
25	254	17.7	186	ADH89336	H. vulgar

HIS at 65

26	249.5	17.4	900	4	ABB62018
27	241	16.8	1013	4	ABB71039
28	240.5	16.8	1069	7	ABB61305
29	240	16.7	358	7	ADB65556
30	237.5	16.6	1142	7	ADC07968
31	232	16.2	160	7	ADH89335
32	232	16.2	160	8	ADG44131
33	232	16.2	4365	6	ABU02252
34	231.5	16.1	149	4	AAH72673
35	230	16.0	1761	4	ABB59512
36	230	16.0	2237	5	ABG70004
37	230	16.0	2703	4	ABB60074
38	229	16.0	158	3	AAI54568
39	229	16.0	2280	4	ABB61650
40	227	15.8	368	4	AAH40299
41	227	15.8	748	4	AAH40299
42	226	15.8	153	3	AAV69495
43	226	15.8	738	5	ABG93140
44	225	15.7	1237	3	AAH81609
45	225	15.7	1428	4	ABB70377

ALIGNMENTS

RESULT 1
AAU01799 standard; protein; 266 AA.
ID AAU01799; (first entry)
XX AAU01799; (first entry)
XX 07-SEP-2001 (first entry)
XX Wheat A-glutinin.
XX Wheat A-glutinin; epitope; coeliac disease; gluten intolerance;
XX T-cell binding; antagonist; transglutaminase; transgenic plant.
XX Triticum aestivum.
XX WO200125793-A2.
XX 12-Apr-2001.
XX 02-OCT-2000; 2000WO-GE003760.
XX 01-OCT-1999; 99GB-00023306.
XX (ISIS-) ISIS INNOVATION LTD.
XX Anderson RP, Hill AVS, Jewell DP;
XX WPI; 2001-300179/31.
XX Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.
XX Claim 1; Page 52; 107pp; English.
The sequence represents wheat A-glutinin. A-glutinin derived peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured. A positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can

[illegible]

XX		SQ	Sequence 266 AA;	
			99.4%; Score 1426; DB 8; Length 266;	
			Best Local Similarity 99.6%; Pred. No. 3.9e-115;	
			Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
QY		1	VRRVPEQLQPNSQQQFEQGVPLVQQQAFPGQQQFPFPGQPYVPQDPFPSQPYLQLQP	60
DY		1	VRRVPEQLQPNSQQQFEQGVPLVQQQAFPGQQQFPFPGQPYVPQDPFPSQPYLQLQP	60
QY		61	FPPHPLPVYQPSFPFGQCPYPQPCQCVSQCPCPPISSQAACQQQQQQQQQQQQQLLQQLLQ	120
DY		61	FPPHPLPVYQPSFPFGQCPYPQPCQCVSQCPCPPISSQAACQQQQQQQQQQQQQLLQQLLQ	120
QY		121	QQLIPCMADVLLQNNINIAHARSQVLQOSTYQLLQELCCQHLMQIPESGCCAIFHVVAII	180
DY		121	QQLIPCMADVLLQNNINIAHARSQVLQOSTYQLLQELCCQHLMQIPESGCCAIFHVVAII	180
QY		181	LHQDQQRQQQQPSSQVSSFQQPLQQYPLGGGSTRPSCNPQAGSTQPPQLQPFETRLAL	240
DY		181	LHQDQQRQQQQPSSQVSSFQQPLQQYPLGGGSTRPSCNPQAGSTQPPQLQPFETRLAL	240
QY		241	QTLPMNCNYIAPYCTIAPFGIGFTN	266
DY		241	QTLPMNCNYIAPYCTIAPFGIGFTN	266
RESULT 3				
AAE38574				
ID	AAE38574	standard; protein; 290 AA.		
XX				
AC	AAE38574:			
DY	04-DEC-2003	(first entry)		
XX				
DE		wheat alpha-2 gliadin protein.		
XX				
KW		wheat; therapy; celiac sprue; dermatitis herpetiformis; gluten toxicity;		
KM		glutenase; foodstuff; antiinflammatory; dermatological; alpha-2 gliadin.		
XX				
OS		Triticum aestivum.		
XX				
PN	WC2003068170-AAZ.			
XX				
PD	21-AUG-2003.			
PV				
PF	14-FEB-2003; 2003WO-US004743.			
PR	14-FEB-2002; 2002US-035723BP.			
PR	14-MAY-2002; 2002US-0380761P.			
PR	28-JUN-2002; 2002US-0392782P.			
PR	31-OCT-2002; 2002US-0422933P.			
PR	20-NOV-2002; 2002US-0428033P.			
PR	20-DEC-2002; 2002US-0435851P.			
PA	(STRD) UNIV IRELAND STANFORD JUNIOR.			
PI	Hausch F, Gray G, Shan L, Khosia C;			
OR	WPI; 2003-657466/66.			

XX The present sequence represents the mature glutenin protein. The DNA
 CC sequence encoding this protein is isolated from the genomic DNA of
 CC Triticum durum L. The gene codes for a low-molecular-weight glutenin
 CC protein and can be used to produce transgenic durum wheat plants with
 CC "better quality characteristics" (no details given). (Updated on 25-MAR-
 CC 2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS
 CC field)
 XX
 XX Sequence 369 AA:
 SO
 Query Match 32.3%; Score 463; DB 2; Length 369;
 Best Local Similarity 40.2%; Pred. No. 1,1e-31;
 Matches 134; Conservative 32; Mismatches 87; Indels 80; Gaps 14;
 6 POLQPNPSSQGP-----QGVPLVQGGPFGQGGQGP--PQGPYPQGPFP-----50
 38 PQGGPSSQGGQGPPLSGGGQGGPFGSQQGGQGPVLPQGSFSGQQQLPFGSQQGGP 97
 51 ---SQGPV-----QLQPPQPHLPYPQPSFPPQ-----PYQPQPGYSQ 89
 98 FSGGGQGVLPQGSFSGQQLPFGSQQGPVLPQGPFGSQQGPFGSQQGPFPFSG 157
 90 PQGGPSSQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQ 132
 158 QGGQGVLPQGGPFGSQQGGQGPVLPQGGPFGSQQGGQGGQGGQGGQGGQGGQGG 216
 133 QH-----NIAHARSQVLAQSTYQLQELCCQHLMOIPFGSQQCOAHNVVHAIIHQGQK 186
 217 QGSPFAMPGSLARSQVLAQSSGCHVMQGCCQQLPQPGQSRVLAIVYSIIL--QEQ 274
 187 QGGQSSQGVFQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQ 234
 275 QGGVSGTCTGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 331
 235 IRLNALQTLPLAMCNVYIAPY--CTIAPFGT 265
 332 MTSIALRTLPKCMWVPLVTRTTRVPGV-GT 363
 RESULT 6
 ADO71669
 ID ADO71669 standard; protein; 297 AA.
 XX
 XX ADO71669;
 XX
 XX 12-AUG-2004 (first entry)
 XX
 XX Amino acid sequence of a modified glutenin LMW subunit.
 DE
 XX low molecular weight subunit; LMW subunit; glutenin;
 KM wheat cultivar Cheyenne; gliadin; flour; tablet; coeliac disease;
 KM gluten intolerance.
 XX
 XX Triticum sp.
 OS
 OS Synthetic.
 XX
 XX EPI42342-A1.
 EN
 XX
 XX 02-JUN-2004.
 DE
 XX
 XX 27-NOV-2002; 2002EP-00026461.
 PR
 XX
 XX 27-NOV-2002; 2002EP-00026461.
 PR
 XX
 XX (BAKE-) BAKEMARK DEUT GMBH.
 PA (MONS) MONSANTO AGRAR DEUT GMBH.
 PA (UNIF-) UNIFERAN GMBH & CO KG.
 PA (PURA-) PURATOS NV.
 XX
 XX Hinzmann E, Wieser H, Stahl U;
 DE
 XX
 XX MPI, 2004-402876/38.

DR N-PSDB; ADO71668.
 XX
 XX Novel nucleic acid comprising sequence encoding modified glutenin
 PT polypeptide, useful for preparing modified glutenin polypeptide as
 PT gliadin substitute in foodstuffs such as dough, pastries and wafers.
 XX
 XX Claim 16; Fig 11; 43pp; English.
 PS
 XX
 XX The present sequence represents a modified low molecular weight (LMW)
 CC subunit of glutenin. The wild type subunit is designated clone LMW6, and
 CC is isolated from wheat cultivar Cheyenne. The LMW6 polypeptide does not
 CC contain the allergenic epitope QQQGP, and shows some minor differences to
 CC published sequences. It therefore represents a new allele for LMW subunit
 CC genes. The LMW6 polypeptide was modified to produce modified glutenin
 CC polypeptides of the invention. In these modified polypeptides one or more
 CC cysteine residues responsible for intermolecular cross linking through
 CC disulfide bridges are deleted or substituted. The modified glutenin
 CC polypeptide is useful as a gliadin substitute. It is also useful in the
 CC preparation of foodstuffs, such as flour or for the preparation of
 CC pharmaceutical products, such as tablets, where the foodstuffs contain a
 CC considerably reduced amount of gliadin proteins or no gliadin proteins.
 CC Pharmaceutical compositions comprising the modified polypeptide of the
 CC invention are useful for treating patients suffering from coeliac disease
 CC or persons who are intolerant to gluten.
 XX
 SO Sequence 297 AA:
 Query Match 31.4%; Score 450.5; DB 8; Length 297;
 Best Local Similarity 41.2%; Pred. No. 1e-30;
 Matches 120; Conservative 38; Mismatches 82; Indels 51; Gaps 13;
 5 VPOLQPNPSSQGGQGVPLVQGGPFGQGGQGPFGPQGPYPQGPFGSQQGPVLPQGP 63
 18 IAQVETSLPGLERMQGQPLQKXETP---QGPSSG---QGGPFGQGPFLQGGPFGSQ 71
 64 PHLFYPQGSFPPQGPYPQGPQVSGQGPISQQAQGGQGGQGGQGGQGGQGGQGG 116
 72 -----GLFSGQKQGPVLPQGPFGSQQGGQGGQGGQGGQGGQGGQGGQGGQ 125
 117 QI-----LQGGQLPFGMDVYLAQHNIHARSQVLAQSTYQLQELCCQHLMOIPFGSQQ 170
 126 QLNPKGVFLQGGQ---GSPVAMPQH---LANSQMWQSSCNVMQGGCCQQLPRIPEGSRYE 179
 171 AIHNVVHAIIHQGQK-----QQGQPSQGV-SFGQPLQ--QYPLGGGSF-----RP 213
 180 AIIAIIISIIHQEGQGQGVFPQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 239
 214 SQGNPQAGSVQPGQQLPQFESIRLALQTLPLAMCNVYIAPYCTI--APFGI 262
 240 QGGQVQKGTFLQPHQIARLEVMYSIARLTLPKCSVNPVLYSITSAPLAV 290
 RESULT 7
 ADH89338
 ID ADH89338 standard; protein; 307 AA.
 XX
 XX ADH89338;
 XX
 XX 06-MAY-2004 (first entry)
 DE
 XX
 XX T. aestivum LMW glutenin-1D1 protein.
 DE
 XX
 XX double stranded RNA; storage protein; 2S-albumen; 7S-globulin;
 KM 11S/12S-globulin; zein-prolamine; homogenitstate metabolic pathway;
 KM pharmaceutical; plant; abiotic stress; fatty acid composition;
 KM lipid composition; oil composition; carbohydrate composition; colour;
 KM pigmentation; pathogen resistance; fruit ripening delay; aging;
 KM male sterility; lignin; fibre; cotton; Vitamin E synthesis; nicotine;
 KM caffeine; theophylline; theanine biosynthesis; glutenin.
 XX
 XX Triticum aestivum.
 OS
 OS WO2003078629-A1.

XX 25-SEP-2003.
 XX 17-MAR-2003; 2003WO-EP002735.
 XX 20-MAR-2002; 2002DE-01012892.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Kock M, Bauer J;
 XX WPI; 2003-803889/75.
 DR N-PSDB; ADH89337.
 XX
 PT Reducing expression of at least two target genes, useful e.g. for
 PT producing transgenic plants, using partly double-stranded interfering
 PT RNA.
 XX
 PS Disclosure; SEQ ID NO 113; 228bp; German.
 XX
 CC This invention describes a novel method for reducing the expression of at
 CC least two different endogenous target genes in a eukaryotic cell or
 CC organism by introducing an RNA molecule that is at least partly double
 CC stranded. The transcribed RNAs from at least two target genes have
 CC homology below 90% and the RNA molecule is formed as a single, self-
 CC complementary molecule. At least one of the double-stranded structures
 CC formed from individual sense sequences has an even number of repeats of
 CC 21 or 22 bp. The RNA molecule may include an intron-encoding sequence. At
 CC least two target genes are selected from different classes of storage
 CC protein genes, i.e. 2S-albumen, 7S- or 11S/12S-globulins or zein-
 CC prolamins and at least one of the sense sequences is identical to storage
 CC protein sequences or genes in the homogenizate metabolic pathway or
 CC enzyme types, e.g. acetyl transacylases, cholesteraes, (de)branching
 CC enzymes or cellulases. The RNA of the invention, also related cassettes,
 CC expression systems, vectors and transgenic organisms are used for
 CC preparation of pharmaceuticals, in biotechnological processes and plant
 CC biotechnology, specifically in plants to improve protection against
 CC abiotic stress, to modify composition and/or content of fatty acids,
 CC lipids and oils, to modify carbohydrate composition, to alter colour or
 CC pigmentation, to reduce content of storage proteins, to increase
 CC resistance to pathogens, to inhibit stem break, to delay fruit ripening
 CC or aging, to induce male sterility, to reduce content of toxic or
 CC unwanted components, to modify lignification and/or lignin content, to
 CC modify the fibre component in foods or fibre quality in cotton, to reduce
 CC susceptibility to shock, to increase synthesis of Vitamin E, to reduce
 CC contents of nicotine, caffeine or theophylline and to increase methionine
 CC content, by reducing threonine, biosynthesis. The method provides a rapid
 CC and efficient way of reducing gene expression, can inhibit more than one
 CC target gene, prevents development of multiple phenotypes (since the
 CC transcription rate is the same for all RNA sequences, significantly
 CC reducing the selection process required to produce an organism with
 CC effective suppression of all target genes), avoids problems of epigenetic
 CC gene silencing, does not require synthesis of individual RNA sequences.
 CC and the method can be applied to plants with complex (polyploid) genomes.
 CC No interference between the individual RNA sequences occur. This sequence
 CC represents a protein encoded by a target gene used in the method of the
 CC invention.
 XX
 XX Sequence 307 AA;
 XX
 XX Query Match 30.6%; Score 439.5; DB 7; Length 307;
 XX Best Local Similarity 42.8%; Pred. No. 9, 4e-30;
 XX Matches 125; Conservative 36; Mismatches 76; Indels 55; Gaps 16;
 XX
 QY 13 PGGGQGGGVPVAVQQGQF-----GGGCGPPGPGQPPGPPGPGPQVQLQGPFPKHP 67
 Db 27 PGERHWQGPPLPPGQPFPGQPIFSQQQD---QQLPFGQPPSSQQP-----PFGQQGPP 78
 QY 68 YPQPGSFPFPPQF-----YFPQPGQYSGPFGQPI---SQQAQGGGQGGGQGGGQGGQ 114
 Db 79 FSGQQGPIILPQPPFSGQQGQLVLVQ-QPPFSQQGQPLPLPQGSBPFGQQGQHQLVQQGIP 137
 QY 115 -LQGLLQGLLPGMDVVLQGH--NTAH---ARSQVLOOSTYQLDLGLCCGHLMDGIPRGS 167

Db 138 WQPSILQGLNPG-KYFLLQGGQSSPAMPGRRLARSQMLQSSCHVWQQGQGLPQIPQOS 196
 QY 168 OCAAHNVVHAITLTHQGGKQGGQSSQVSPFGQPLQGYPLQGSFPPSPGQNPQ----- 219
 Db 197 RYEAIRAITYSIIL--QEGQYVQGSILQSGQQGPPQ---LGGCVSQPQQGSQQQLGQPPQ 251
 QY 220 ---AGGS-VQPGQPLQPFERINLAIQTLPAMCNVYIAP--CTIAPFGIGT 265
 Db 252 CQLAQGTFLQPHQIAQLEWMTSIALRLIPTMCSSVNPVPLKRTTSVFEVGT 302
 XX
 XX RESULT 8
 XX ADG44134
 XX ID ADG44134 standard; protein, 307 AA.
 XX AC
 XX ADG44134;
 XX
 XX 26-FEB-2004 (first entry)
 XX
 XX T. aestivum glutenin-1D1 protein.
 XX
 XX oil content; plant; storage protein; seed-specific promoter; 2S-albumin;
 XX 7S-globulin; 11S-globulin; 12S-globulin; zein-prolamins; transgenic;
 XX oil production; fat production; free fatty acid production; food;
 XX animal feed; pharmaceutical; fine chemical production; glutenin.
 XX
 XX Triticum aestivum.
 XX
 XX WO2003077643-A2.
 XX
 XX 25-SEP-2003.
 XX
 XX 17-MAR-2003; 2003WO-EP002733.
 XX
 XX 20-MAR-2002; 2002DE-01012893.
 XX
 XX (BADI) BASF PLANT SCI GMBH.
 XX
 XX Bauer J;
 XX WPI; 2004-011485/01.
 DR N-PSDB; ADG44133.
 XX
 PT Increasing total oil content of plants, useful e.g. as foods or animal
 PT feeds, by reducing amount of storage proteins, particularly with double-
 PT stranded interfering RNA.
 XX
 XX Claim 4; SEQ ID NO 174; 253bp; German.
 XX
 CC This invention describes a novel method for increasing the total oil
 CC content of a plant by reducing the amount of at least one storage protein
 CC in the plant (or its tissue, organs, parts or cells) and selecting plants
 CC that have higher total oil content than starting plants. The storage
 CC protein is suppressed by introducing antisense RNA, optionally combined
 CC with a ribozyme, sense RNA that induces co-suppression, DNA-binding
 CC factors directed against storage protein genes, viral sequences that
 CC degrade storage protein RNA, constructs that induce homologous
 CC recombination of endogenous storage protein genes or mutations into
 CC storage protein genes. Most preferably a plant cell is stably transfected
 CC with a recombinant expression construct, then regenerated to plants that
 CC express the incorporated sequence. The expression constructs particularly
 CC contain a seed-specific promoter and they are introduced into plants by
 CC standard methods, e.g. via Agrobacterium. The preferred storage proteins
 CC of the invention are 2S-albumens, 7S or 11S/12S-globulins or zein-
 CC prolamins. Transgenic organisms produced by the new methods are used for
 CC production of oils, fats, free fatty acids or their derivatives, useful
 CC as foods, animal feeds, pharmaceuticals and fine chemicals. This sequence
 CC represents a storage protein used to illustrate the method of the
 CC invention.
 XX
 XX Sequence 307 AA;
 XX

DR N-PSDB; ABL15798.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 41877; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences
 XX
 SQ Sequence 1798 AA;

Query Match 20.3%; Score 290.5; DB 4; Length 1798;
 Best Local Similarity 37.5%; Pred. No. 5.5e-16;
 Matches 100; Conservative 18; Mismatches 94; Indels 55; Gaps 12;

QY 3 VPVPLQPCNP-SQQQPCQEVPLVQ-----QQQPCQCCQFPFPOQ 41
 Db 264 VPGATQPCQSFSSQKPIPTDPVAVQVLSRSALSSNODSLMRQQLKXCCQMQCQ 323
 QY 42 PYPQPCPPF-SQQPPLQLPFP-CPHLPYPQ--PQSFPPQCPYPQPCQSPQCPISQ 97
 Db 324 MAPCQCCQCCQWQPCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 382
 QY 98 QACCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 153
 Db 383 QCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 440
 QY 154 ELCCGHLWQIPESQCAIHNVVHAILHQQCKQCCQCCQCCQCCQCCQCCQCCQCCQ 213
 Db 441 -----ALQKCCQ-----LHVVQCAQCCQCCQCCQCCQCCQCCQCCQCCQ 481
 QY 214 SQQNPQAGSVQPCQLPQFETRNAL 240
 Db 482 QGHVQCCQ--QPCQV-QTCCQCCQAL 504

RESULT 11

AB63057
 ID ABB63057 standard; protein, 2285 AA.

XX ABB63057;
 AC
 XX
 DT 26-MAR-2002 (first entry)
 DE Drosophila melanogaster polypeptide SEQ ID NO 15963.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PMD, Myers EW;

XX WPI: 2001-656860/75.
 DR N-PSDB; AB107160.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 15963; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences
 XX
 SQ Sequence 2285 AA;

Query Match 18.9%; Score 271; DB 4; Length 2285;
 Best Local Similarity 35.7%; Pred. No. 3.5e-14;
 Matches 101; Conservative 14; Mismatches 104; Indels 64; Gaps 13;

QY 7 QLPQPCNP-----SQQPCQEVPLVQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 54
 Db 909 QMCCQCPVAVPYNHVMQCCQVN--QQCCQCPVMQQLPQVQVQCPVLPPOPHECCP 966
 QY 55 YQLQPCFPQ-----PMLPYPQCCFPFPQCPYPQPCQSPQCPISQCCQ 99
 Db 967 QCCQCCPLCCQLLQQLVHNVQAPDL--TCCQCAQCCQCCQCCQCCQCCQCCQCCQCCQ 1024
 QY 100 QCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 153
 Db 1025 QCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 1084
 QY 154 ELCCGHLWQIPESQCAIHNVVHAILHQQCKQCCQCCQCCQCCQCCQCCQCCQCCQ 204
 Db 1085 QCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQCCQ 1141
 QY 205 PL-----GGSFPPSQNPQAGSVQPCQLPQF 232
 Db 1142 PPTSVAPPIQHTYNGCGGVTLSDAQCCQHPGSAVFPQCAPP 1184

RESULT 12

AA96255
 ID AA96255 standard; protein, 1162 AA.

XX AA96255;
 AC
 XX
 DT 12-SEP-2003 (revised)
 DE 11-SEP-2000 (first entry)
 XX
 KW Kaposi's sarcoma-associated herpesvirus LANA.
 XX
 KW Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
 KW latency-associated nuclear antigen; LANA; gamma-herpes virus;
 KW Human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE;
 KW Kaposi's sarcoma; primary effusion lymphoma; PEL;
 KW human immunodeficiency virus; HIV; multicentric Castleman's disease.
 XX
 OS Human herpesvirus 8.
 XX
 FH Key
 FT 14.17 Location/Qualifiers
 FT Domain
 FT 64..70 /note="nuclear localisation signal, NLS"
 FT Domain
 FT 320..429 /note="nuclear localisation signal, NLS"
 FT Region


```

Db      664 EQQDD-----EQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQD 718
Cy      230 PPFEE 234
      1 ::
Db      717 EQQQD 721

RESULT 13
ID      AAY58500
AC      AAY58500 standard; protein; 1162 AA.
XX
XX      AAY58500;
XX
XX      06-AUG-2003 (revised)
DT
DT      10-APR-2000 (first entry)
XX
XX      HHV8 ORF 73 protein, SEQ ID NO:21.
DE
XX      HHV8, detection; diagnosis; Kaposi's sarcoma; AIDS; immunogen; antigen.
XX
XX      Human herpesvirus 8.
XX
XX      Key Location/Qualifiers
FH
FH      Misc-difference 96
FT
FT      /label= unknown
ET
XX      WO9961909-A2.
XX
XX      02-DEC-1999.
XX
XX      26-MAY-1999; 99NC-US011407.
XX
XX      26-MAY-1998; 98US-0086655P.
XX
XX      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX      Pau C;
XX
XX      WPI; 2000-097142/08.
XX
XX      New methods and compositions for the detection of human herpesvirus.
XX
XX      Claim 2; Page 59-62; 68pp; English.
XX
XX      Sequences AAY58480-Y58532 represent immunogenic polypeptides derived from
CC      human herpes virus type 8 (HHV8, a gammaherpesvirus). HHV8 plays an
CC      important role in the pathogenesis of AIDS-related Kaposi's sarcoma. The
CC      invention relates to a novel method of detecting the presence of human
CC      herpesvirus 8 in a biological sample using peptides representative of
CC      dominant antigenic regions of HHV8. The method comprises contacting one
CC      or more isolated, immunogenic HHV8 peptides with an antibody-containing
CC      biological sample, and detecting the formation of a complex between the
CC      peptide and the antibody. The presence of a peptide-antibody complex
CC      indicates the presence of human herpesvirus 8. The detection of HHV8
CC      infection can be used to diagnose AIDS-associated Kaposi's sarcoma. The
CC      HHV8-specific antibodies are useful therapeutically when for the passive
CC      immunisation of a human against HHV8 infection, thereby reducing HHV8
CC      related disease. The detection assays are highly specific, sensitive and
CC      accurate. Early detection and treatment of Kaposi's sarcoma could
CC      diminish the severity of symptoms related to AIDS and the sensitive
CC      techniques could reduce erroneous characterisations of skin disorders.
CC      Previous assays for HHV8 antibodies such as immunofluorescence assays,
CC      immunoblots and enzyme immunoassays lack the sensitivity and accuracy
CC      needed for reliable diagnosis of Kaposi's sarcoma. Further advantages of
CC      the assays are that reproducible results are obtained and the method is
CC      suitable for rapid throughput and screening of samples economically.
CC      (Updated on 06-AUG-2003 to correct OS field.)
XX
XX      Sequence 1162 AA;
SQ

Query March 16.7%; Score 268; DB 3; Length 1162;
Best Local Similarity 38.0%; Pred. No. 2.9e-14;
Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

```


QY 4 PVFQLQPNPSQQQGEVPLVQ---QQQFPGQ---QQFPQQPYPQPFPSQQPYLQLQ 59
 Db 495 PLOEPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGE 553
 QY 60 P---FPQPHLPY---PQ---PQSFPQQPYPQPF-QPQYSQQQPFISQQQAQQQQQQQQQQ 109
 Db 554 PQQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQ 613
 QY 110 QQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQ 169
 Db 614 EQQDEQQQDEQQ---QDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 663
 QY 170 QAIHNVHAIIILHQQKQCCQSSQVSFQCPQLQYPLQGGSFRPSQQNPAQGSVQPQL 229
 Db 664 EQQGD-----EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 716
 QY 230 PQFEE 234
 Db 717 EQQGD 721

RESULT 14

AAB62331
 ID AAB62331 standard, protein, 1162 AA.

AC AAB62331;

DT 06-AUG-2003 (revised)
 DT 29-JUN-2001 (first entry)

DE Amino acid sequence of KSHV tethering protein LANA.

KM Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis;
 KM Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;
 KM KSHV; latency-associated nuclear antigen; LANA.

OS Human herpesvirus 8.

PN WO200125484-A2.

PD 12-APR-2001.

PF 29-SEP-2000; 2000WO-US026908.

PR 01-OCT-1999; 99US-00410399.

PA (UNMI) UNIV MICHIGAN.

PI Robertson ES, Cotter MA;

XX WPI; 2001-281736/29.

DR N-PSDB; AAF82301.

PT A composition for use in gene therapy comprises an expression vector that
 PT includes a nucleic acid sequence encoding a nucleic acid binding protein.

PS Disclosure; Fig 9B; 60pp; English.

CC The invention provides a composition comprising nucleic acid, histone H1
 CC protein and expression vector operationally encoding a protein suitable
 CC for tethering the nucleic acid to the histone H1 protein, where the
 CC tethering protein is LANA. The composition is useful in aiding the
 CC retention of the viral DNA in the host cell. The viral vector encodes a
 CC protein suitable for tethering DNA to Histone H1. Methods for screening of
 CC for compounds which are agonistic or antagonistic for the tethering of
 CC viral proteins to histone H1 and DNA binding sites are useful for
 CC developing the method of viral transfer. The composition has applications
 CC to gene therapy, including the treatment of multiple sclerosis
 CC Parkinson's disease, Huntington disease and diabetes. The present
 CC sequence represents the amino acid sequence of the Kapost's sarcoma
 CC associated herpesvirus (human herpesvirus 8) latency-associated nuclear
 CC antigen (LANA), which acts as a tethering protein. (Updated on 06-AUG-

CC 2003 to correct CS field.)

XX Sequence 1162 AA;

SQ Query Match 18.7%; Score 268; DB 4; Length 1162;

Best Local Similarity 38.0%; Pred. No. 2.9e-14;

Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

QY 4 PVFQLQPNPSQQQGEVPLVQ---QQQFPGQ---QQFPQQPYPQPFPSQQPYLQLQ 59
 Db 495 PLOEPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGEPPQQGE 553
 QY 60 P---FPQPHLPY---PQ---PQSFPQQPYPQPF-QPQYSQQQPFISQQQAQQQQQQQQQQ 109
 Db 554 PQQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQ 613
 QY 110 QQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQ 169
 Db 614 EQQDEQQQDEQQ---QDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 663
 QY 170 QAIHNVHAIIILHQQKQCCQSSQVSFQCPQLQYPLQGGSFRPSQQNPAQGSVQPQL 229
 Db 664 EQQGD-----EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 716
 QY 230 PQFEE 234
 Db 717 EQQGD 721

RESULT 15

ABB05621
 ID ABB05621 standard, protein, 1162 AA.

AC ABB05621;

DT 25-APR-2002 (first entry)

DE Kapost's sarcoma-associated herpesvirus LANA protein.

XX Kapost's sarcoma-associated herpesvirus; KSHV; LANA; RVCAE; PEL;
 KM KSHV terminal repeat; rhadino virus cis acting element; episome;
 KM primary effusion lymphoma; latency-associated nuclear antigen;
 KM gene therapy; gene transfer.

OS Human herpesvirus 8.

PN US6322792-B1.

PD 27-NOV-2001.

PF 21-APR-1999; 99US-00298568.

PR 19-NOV-1998; 98US-0109422P.

PA (KIEF/) KIEFF E D.

PI Kieff ED, Ballestas ME, Kaye KM;

XX WPI; 2002-153769/20.

DR N-PSDB; ABA93487.

PT System for episomal retention of plasmids in mammalian cells, useful in
 PT gene therapy, comprises rhadinoviral LANA and RVCAE sequences.

PS Disclosure; Fig 7; 27pp; English.

XX The present invention describes a system (A) for maintaining a plasmid as
 CC an episome in mammalian cells, comprising the rhadinoviral sequence LANA
 CC (latency-associated nuclear antigen) of 3489 base pairs (see ABA93487,
 CC S1) expressed in the cell, and the rhadinoviral sequence RVCAE
 CC (rhadinoviral cis-acting element) of 801 base pairs (see ABA93488, S2)
 CC present in the plasmid. Also described is a method for maintaining a
 CC closed circular DNA in a cell by expressing (S1) in the cells and having

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OM protein - protein search, using sw model

Run on: December 14, 2004, 17:06:20 ; Search time 19 Seconds

(without alignments)
928.452 Million cell updates/sec

Title: US-10-089-700-3-H65

Perfect score: 1434

Sequence: 1 VRVVPQIQPNPSCQPPQF.....CNVYIAPYCTIAPGIRGTM 266

Scoring table:

BLOSUM62

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463	32.3	369	2	US-08-991-300-2
2	268	18.7	1162	2	US-08-728-323A-2
3	268	18.7	1162	3	US-09-298-568-2
4	268	18.7	1162	4	US-09-410-399-2
5	268	18.7	1162	4	US-09-894-273-2
6	248	17.3	788	2	US-08-918-914-4
7	235.5	16.4	256	4	US-09-248-796A-1251
8	234	16.3	579	4	US-09-270-767-45042
9	224	15.6	494	4	US-09-668-119-3
10	216	15.1	2074	4	US-09-491-356C-9
11	201	14.0	2023	4	US-09-491-356C-8
12	201	14.0	2124	4	US-09-538-092-1377
13	198.5	13.8	505	4	US-09-248-796A-19253
14	197.5	13.8	663	4	US-09-270-767-61220
15	197.5	13.8	1591	4	US-09-270-767-45698
16	197.5	13.8	2441	1	US-08-194-468-2
17	197.5	13.8	2441	3	US-08-961-739-2
18	197.5	13.8	2441	3	US-09-514-247A-8
19	197.5	13.8	2441	4	US-09-686-316-2
20	196.5	13.7	379	4	US-09-248-796A-23759
21	196.5	13.7	729	3	US-09-625-188-20
22	196.5	13.7	2442	4	US-09-514-247A-10
23	196.5	13.7	2442	4	US-09-538-092-1370
24	196	13.7	216	4	US-09-248-796A-21017
25	187	13.0	295	4	US-09-248-796A-20004
26	186.5	13.0	169	4	US-09-248-796A-28087
27	186.5	13.0	320	4	US-09-248-796A-24758

28	184.5	12.9	316	4	US-09-270-767-42663	Sequence 42663, A
29	184.5	12.9	332	4	US-09-248-796A-21649	Sequence 21649, A
30	183	12.8	261	4	US-09-602-565-34	Sequence 34, Appl
31	183	12.8	519	4	US-09-248-796A-19263	Sequence 19263, A
32	179	12.5	408	4	US-09-248-796A-14480	Sequence 14480, A
33	178	12.4	383	4	US-09-248-796A-23235	Sequence 23235, A
34	178	12.4	657	4	US-09-248-796A-19232	Sequence 19232, A
35	178	12.4	1319	4	US-09-538-092-1291	Sequence 1291, Ap
36	176.5	12.3	107	4	US-09-668-119-6	Sequence 6, Appl
37	176.5	12.3	684	4	US-09-823-240A-9	Sequence 9, Appl
38	176	12.3	618	4	US-09-248-796A-15319	Sequence 15319, A
39	176	12.3	848	4	US-09-538-092-33	Sequence 33, Appl
40	176	12.3	1507	4	US-09-914-259-37	Sequence 37, Appl
41	174.5	12.2	382	4	US-09-248-796A-18720	Sequence 18720, A
42	173.5	12.1	2781	4	US-09-698-295-10	Sequence 10, Appl
43	171.5	12.0	903	2	US-08-853-310-2	Sequence 2, Appl
44	171	11.9	675	4	US-09-248-796A-20699	Sequence 20699, A
45	170.5	11.9	311	4	US-09-248-796A-27827	Sequence 27827, A

ALIGNMENTS

RESULT 1
US-08-991-300-2
Sequence 2, Application US/08991300
Patent No. 5973225
GENERAL INFORMATION:
APPLICANT: D'OVIDIO, RENATO
APPLICANT: PORCEDDU, ENRICO
APPLICANT: MERCHITELLI, CINZIA
APPLICANT: CARDELLI, LUISA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,300
FILING DATE: 16-DEC-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-0201-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-300-2
Query Match 32.3%; Score 463; DB 2; Length 369;
Best Local Similarity 40.2%; Pred. No. 8,1e-35;

Matches 134; Conservative 32; Mismatches 87; Indels 80; Gaps 14;

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QY 6 PQLQPNPSQQP-----QEVVPLVQQQPPGQQQQP--PQDPYPPQPP----- 50
Db 38 PQQQPCSCQQQPPPLSQQQQPPPSQQQPPPSQQQPPVLPQDPSSQQQLPPSSQQQPP 97
QY 51 ---SQEYL-----QLQPPQPHLPYPPQSPFPQ-----PYPPQPPQYSC 89
Db 98 FSGQQQPPVLPQPSFSQQQLPPPSQQQLPPPSQQQLPPPSQQQLPPPSQQQLPPFSQ 157
QY 90 PQQPISQQQAQQQQQQQ-----QQQQQQQIQQ-----ILQQQLPPQMDVVLQ 132
Db 158 QQQPVLPPQPPPSQQQPPPIPPQPPPSQQQPPVLLQQQIPVHPSILQQQLNQC-KVFLQ 216
QY 133 QH-----NTAHASQVLTQSTYQLQELCCQHLAQIPQSQCCQALHNVAIILHQQK 186
Db 217 QQQSPAMPPQSLARSQVLQSSSCHVWQQCCQQLPQIPQPSRYEALRAIVYSIL--QEQ 274
QY 187 QQQQSSQVSFPQPLQYPLQGSFRPSQNPQAQS-----VQPPQLPQFE 234
Db 275 QQVQSGSIGTQQQQPPQ---LGQCVSQPQQQSCQQLGQQPQQQQLAHGTF-LPHQLAQLEV 331
QY 235 IRLNALQTLPMACNVVIAFY--CTIAPFGIFGT 265
Db 332 MTSIALRKLPMCMWNVPLVYRTTRVPFSV-GT 363
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RESULT 2

US-08-728-323A-2

Sequence 2, Application US/08728323A

Patent No. 5948676

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Bohenzky, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Edelman, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: Immediate Early Protein From Kaposi's

TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA

TITLE OF INVENTION: Encoding Same And Uses Thereof

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent'n Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728,323A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/52268/JPM/MSC/SKS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEPHONE: 212-391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1162 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-728-323A-2

Query Match

18.7%; Score 268; DB 2; Length 1162;

Best Local Similarity 38.0%; Pred. No. 2.8e-16;
Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

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QY 4 PVPQLQPNPSQQQPPQEVPLVQ--QQQFPQQQ--QQFPQPPYPPQPPPSQQPYLQLQ 59
Db 495 PLSPPQDDEPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 553
QY 60 P---FPQPHLY---PQ---PQSPFPQPPYPPQ-QPPYSPQPPPISSQQAQQQQQQQQ 109
Db 554 PQQREPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 613
QY 110 QQQQLLQQQLIPCDVVLQCHNIAHASQVLTQSTYQLQELCCQHLAQIPQSQCC 169
Db 614 EQQDDEQQDDEQQ---QDEQQDDEQQDDEQQDDEQQDDEQQDDE---QQDDEQQD 663
QY 170 QAINHVVAIILHQQKQCCQPPSSQVSFPQPLQYPLQGSFRPSQNPQAQSVQPPQL 229
Db 664 EQQD-----EQQDDEQQDDEQQDDEQQDDEQQDDEQQDDEQQDDEQQDDEQQD 716
QY 230 PPFEE 234
Db 717 EQQD 721
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RESULT 3

US-09-298-568-2

Sequence 2, Application US/09298568

Patent No. 6322792

GENERAL INFORMATION:

APPLICANT: Kieff, Elliott D.

APPLICANT: Ballestas, Mary E.

APPLICANT: Kaye, Kenneth M.

TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO

TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE

FILE REFERENCE: 16412-1001R

CURRENT APPLICATION NUMBER: US/09/298,568

EARLIER FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,422

EARLIER FILING DATE: 1998-11-19

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patent'n Ver. 2.0

SEQ ID NO 2

TYPE: PRT

ORGANISM: Kaposi's sarcoma-associated herpesvirus

US-09-298-568-2

Query Match 18.7%; Score 268; DB 3; Length 1162;

Best Local Similarity 38.0%; Pred. No. 2.8e-16;

Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

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QY 4 PVPQLQPNPSQQQPPQEVPLVQ--QQQFPQQQ--QQFPQPPYPPQPPPSQQPYLQLQ 59
Db 495 PLSPPQDDEPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 553
QY 60 P---FPQPHLY---PQ---PQSPFPQPPYPPQ-QPPYSPQPPPISSQQAQQQQQQQQ 109
Db 554 PQQREPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 613
QY 110 QQQQLLQQQLIPCDVVLQCHNIAHASQVLTQSTYQLQELCCQHLAQIPQSQCC 169
Db 614 EQQDDEQQDDEQQ---QDEQQDDEQQDDEQQDDEQQDDEQQDDE---QQDDEQQD 663
QY 170 QAINHVVAIILHQQKQCCQPPSSQVSFPQPLQYPLQGSFRPSQNPQAQSVQPPQL 229
Db 664 EQQD-----EQQDDEQQDDEQQDDEQQDDEQQDDEQQDDEQQDDEQQDDEQQD 716
QY 230 PPFEE 234
Db 717 EQQD 721
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RESULT 4

US-09-410-399-2
; Sequence 2, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; TITLE OF INVENTION: Methods to inhibit or Enhance the Binding of Viral DNA
; FILE REFERENCE: US-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-2

Query Match 18.7%; Score 268; DB 4; Length 1162;

Best Local Similarity 38.0%; Pred. No. 2.8e-16;
Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

QY 4 PVPOLQPNPQQQPPQEQVPLVQ--QQQPPGQQ--QQPFPQPPQPPQPPFPQPPVQLQ 59
DB 495 PLOEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEP 553
QY 60 P---FPQPHLY---PQ---PQSFPQPPQPPQ--QPQISQPPQPPQPPQPPQPPQPPQ 109
DB 554 PQQREPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 613
QY 110 QQQQILQQQLPCMDVVLQGNHIAHSQVLCSTYQLLELCCQHLMQIPESQC 169
DB 614 EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 663
QY 170 QAINHVHAILHQQQKQQQSSQVSFQPLQYPLQGSGFRPQQNPQAGSVQPPQL 229
DB 664 EQQQD-----EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQD 716
QY 230 PQEE 234
DB 717 EQQQD 721

RESULT 5

US-09-894-273-2
; Sequence 2, Application US/09894273
; Patent No. 6756203
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Balleslas, Mary E.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; FILE REFERENCE: 16412-1001R
; CURRENT APPLICATION NUMBER: US/09/894,273
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/109,422
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-2

Query Match 18.7%; Score 268; DB 4; Length 1162;

Best Local Similarity 38.0%; Pred. No. 2.8e-16;
Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

QY 4 PVPOLQPNPQQQPPQEQVPLVQ--QQQPPGQQ--QQPFPQPPQPPQPPFPQPPVQLQ 59

DB 495 PLOEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEP 553
QY 60 P---FPQPHLY---PQ---PQSFPQPPQPPQ--QPQISQPPQPPQPPQPPQPPQPPQ 109
DB 554 PQQREPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 613
QY 110 QQQQILQQQLPCMDVVLQGNHIAHSQVLCSTYQLLELCCQHLMQIPESQC 169
DB 614 EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDE 663
QY 170 QAINHVHAILHQQQKQQQSSQVSFQPLQYPLQGSGFRPQQNPQAGSVQPPQL 229
DB 664 EQQQD-----EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQD 716
QY 230 PQEE 234
DB 717 EQQQD 721

RESULT 6

US-08-918-914-4
; Sequence 4, Application US/08918914
; Patent No. 5878963
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Peter
; APPLICANT: Hutchinson, Nancy
; APPLICANT: Lawton, Michael
; APPLICANT: Magna, Holly
; APPLICANT: Yocum, Sue
; TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,914
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1070094
US-08-918-914-4

Query Match 17.3%; Score 248; DB 2; Length 788;

Best Local Similarity 31.0%; Pred. No. 1.2e-14;
Matches 89; Conservative 23; Mismatches 97; Indels 78; Gaps 10;

QY 2 RVNPPQLQ-----PQNSQQQPPQEVPLVQQQQPPQGGQQPPPPQPPQPPPPPPPPPP 55
 DB 201 RVAPAPACQYAPRAPPYPSACQ-----QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 252
 QY 56 LQAPPPPPPLPP 115
 DB 253 QQQQQQQQQPP 311
 QY 116 QQQQQQQQQPP 175
 DB 312 QQQQQQQQQPP 342
 QY 176 VHHLLHQQQ 212
 DB 343 -----PQQQQPP 396
 QY 213 PQQQQPP 259
 DB 397 PVPQAPQGE---RTPPPVLAIVNTATQ---PPLPPPPPPPPPPPPPPPPPPPPPP 438

RESULT 7

US-09-248-796A-21251
 Sequence 21251, Application US/09248796A
 Patent No. 6747137
 GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

FILE REFERENCE: 107196.132
 CURRENT APPLICATION NUMBER: US/09/248,796A
 CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
 PRIOR FILING DATE: 1998-02-13
 PRIOR APPLICATION NUMBER: US 60/096,409
 PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 21251

LENGTH: 256
 TYPE: PRT
 ORGANISM: Candida albicans
 FEATURE:
 NAME/KEY: UNSURE
 LOCATION: (250)
 OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno

US-09-248-796A-21251
 Query Match
 Best Local Similarity 38.1%; Score 235.5; DB 4; Length 256;
 Matches 74; Conservative 9; Mismatches 68; Indels 43; Gaps 8;

QY 38 PQQPP 97
 DB 75 PQQPP 126
 QY 98 QQQ 157
 DB 127 QQQ 164
 QY 158 QHLLQIPBQSCQAHHVVVVAHLLHQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 217
 DB 165 QHVKQ 212
 QY 218 PQAQGSVPPQQLPQ 231
 DB 213 -QLVGRSPQPSFPQ 225

RESULT 8

US-09-270-767-45042

Sequence 45042, Application US/09270767
 Patent No. 6703491
 GENERAL INFORMATION:

APPLICANT: Homburger et al.
 TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 FILE REFERENCE: File Reference: 7326-094
 CURRENT APPLICATION NUMBER: US/09/270,767
 CURRENT FILING DATE: 1999-03-17
 NUMBER OF SEQ ID NOS: 62517
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 45042
 LENGTH: 498
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 FEATURE:
 OTHER INFORMATION: Xaa means any amino acid
 US-09-270-767-45042

Query Match
 Best Local Similarity 32.1%; Score 234; DB 4; Length 498;
 Matches 99; Conservative 20; Mismatches 101; Indels 88; Gaps 15;

QY 6 PQLPPQNP-SQQPPQEGVPLVQQQQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 57
 DB 181 PQLPPQNP-SQQPPQEGVPLVQQQQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 235
 QY 58 ---LQPPPPPPPLPP 105
 DB 236 WQELRQPPQDFQLAPNTS--PPQ---QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 291
 QY 106 QQQ 151
 DB 292 QQQ 348
 QY 152 LQELCCQHMLPP 208
 DB 349 LVETQHGHV---QKQ---HQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 386
 QY 209 GSFRPQQNPQA-----QGSVPQQLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 257
 DB 387 HTMPPPQTSPPVYVTSPLLEQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 440
 QY 258 APFGIFGT 265
 DB 441 TPTGIAS 448

RESULT 9

US-09-668-119-3

Sequence 3, Application US/09668119
 Patent No. 6768303
 GENERAL INFORMATION:

APPLICANT: Solomon, William B
 TITLE OF INVENTION: Transcriptional adaptor protein

FILE REFERENCE: 011,0250
 CURRENT APPLICATION NUMBER: US/09/668,119
 CURRENT FILING DATE: 2000-09-22
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 3

LENGTH: 579
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-668-119-3

Query Match
 Best Local Similarity 34.8%; Score 224; DB 4; Length 579;
 Matches 92; Conservative 11; Mismatches 87; Indels 74; Gaps 11;

QY 8 LQPPPPPPPLPP 65
 DB 134 LQPPPPPPPLPP 193
 QY 66 LPYPQGSFPQPP 125

Db 194 LITLHKN---QQQIQQQQQQ---QRIAGLQLQQQQQQQQQQQQ---QALHQA--- 241
 QY 126 CNDVLIQAHNIHARSQVLIQSTYQLLQELCCQHLWQIPESQCCQAHNVHAILLHQ 185
 Db 242 -----PPIQCPMPQPPPPSQAIPQ-----QLQMHHTQH---HQPP 276
 QY 186 KQQQSSQVSSFCQPLQQY-----LQCGSFPSQ-----QNPQAQ 221
 Db 277 PQQCP--FYAKQVPSQLPQSQCTQPLVSQAALGQMLYTPPLKPYARMVYQCPVQ 334
 QY 222 GSVQPOQLPQFEIRNLALQTLPA 245
 Db 335 PQVQQQ-----TAVQTAQA 349

RESULT 10
 US-09-491-356C-9
 ; Sequence 9, Application US/09491356C
 ; Patent No. 6586061
 ; GENERAL INFORMATION:
 ; APPLICANT: Philibert, Robert A.
 ; APPLICANT: Gims, Edward I.
 ; APPLICANT: Delist, Lynn
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13
 ; FILE REFERENCE: 9465, 6US11
 ; CURRENT APPLICATION NUMBER: US/09/491,356C
 ; CURRENT FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/083,465
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 9
 ; LENGTH: 2074
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 ; US-09-491-356C-9

Query Match 15.1%; Score 216; DB 4; Length 2074;
 Best Local Similarity 30.6%; Pred. No. 3,5e-11;
 Matches 87; Conservative 15; Mismatches 90; Indels 92; Gaps 10;

QY 7 QLOPQNPSSQCPQEQVPLVQQQFPQQ--QCPFPQCPY-----PQPPPPSQCPY 55
 Db 1807 QQQPVPQGGRLKQ--LQSSQGLQSSVHQMTSSSYGLQTSQSPSLQGYTSVSH 1864
 QY 56 LQCPFPQPHLPYPCQSPFPQCPYPOQPOYSQ----- 89
 Db 1865 VGLQHTGADPRHILQCRPSGVH-QCAPYGHGLJTSQFSHQTLQCTPMGTMTPLS 1923
 QY 90 -----PQPPISQQAQAAAAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 135
 Db 1924 AGQAGVSTSLPQQ 1973
 QY 136 IAHARSQVLIQSTYQLLQELCCQHLWQIPESQCCQAHNVHAILLHQKQKQKQKQKQKQ 195
 Db 1974 --HRRQQQQQ-----QMLRQAAAAQQQQ-----QQQQQQQQQQQQQQ 2009
 QY 196 SFPQPLQCPYPLQGGSRPSQNPQAGSVQPPQLPQFEIRNL 239
 Db 2010 QQQQPFHQ-----QQAPPPQPPQSPQCFQGGIQQTQQQQQQTA 2049

RESULT 11
 US-09-491-356C-8
 ; Sequence 8, Application US/09491356C
 ; Patent No. 656061
 ; GENERAL INFORMATION:
 ; APPLICANT: Philibert, Robert A.
 ; APPLICANT: Gims, Edward I.
 ; APPLICANT: Delist, Lynn
 ; TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13

FILE REFERENCE: 9465, 6US11
 ; CURRENT APPLICATION NUMBER: US/09/491,356C
 ; CURRENT FILING DATE: 2000-01-26
 ; PRIOR APPLICATION NUMBER: PCT/US99/09365
 ; PRIOR FILING DATE: 1999-04-29
 ; PRIOR APPLICATION NUMBER: 60/083,465
 ; PRIOR FILING DATE: 1998-04-29
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 2023
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-491-356C-8

Query Match 14.0%; Score 201; DB 4; Length 2023;
 Best Local Similarity 29.2%; Pred. No. 8,1e-10;
 Matches 87; Conservative 15; Mismatches 90; Indels 106; Gaps 11;

QY 7 QLOPQNPSSQCPQEQVPLVQQQFPQQ--QCPFPQCPY----- 43
 Db 1747 QQQPVPQGGRLKQ--LQSSQGLQSSVHQMTSSSYGLQTSQSPSLQGYTSVSH 1804
 QY 44 --PQPPFPSPQCPYQLQFPQPHLPY-----QPSFPQCPY----- 81
 Db 1805 GPAGTVPSPSSQCPYSTPSTNPLVDPTRHLQCRPSGVHQAAPYGHGLJTSQFS 1864
 QY 82 --QPOPOYSQ-----PQPPISQQAQAAAAQQQQQQQQQQQQQQQQQQQQQQQQQQ 117
 Db 1865 HQTLLQCTPMSTMTMPSAGVAGVSTALPQQQQQQQQQQQQQQQQQQQQQQQQQQ 1924
 QY 118 --LQCGLPCMDVLIQAHNIHARSQVLIQSTYQLLQELCCQHLWQIPESQCCQAHNV 176
 Db 1925 HIRQQ-----QQQLRQAAAAQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 1962
 QY 177 HAILLHQKQKQKQ-----QPSQVSPQ-QPLQCPYPLQGGSRPSQNPQAGSVQPPQ 227
 Db 1963 -----HQQQQQQQQAPPPQPPQSPQCFQGGIQQTQQQQQQTAALVRLQQLSNTQ 2015

RESULT 12
 US-09-538-092-1377
 ; Sequence 1377, Application US/09538092
 ; Patent No. 6753314
 ; GENERAL INFORMATION:
 ; APPLICANT: Gloc, Loic
 ; APPLICANT: Mansfield, Traci A.
 ; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
 ; FILE REFERENCE: 15966, 542
 ; CURRENT APPLICATION NUMBER: US/09/538,092
 ; CURRENT FILING DATE: 2000-03-29
 ; PRIOR APPLICATION NUMBER: 60/127,352
 ; PRIOR FILING DATE: 1999-04-01
 ; PRIOR APPLICATION NUMBER: 60/178,365
 ; PRIOR FILING DATE: 2000-02-01
 ; NUMBER OF SEQ ID NOS: 1387
 ; SOFTWARE: CurateSeqFormat Version 0.9
 ; SEQ ID NO 1377
 ; LENGTH: 2124
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; LOCATION: (0)...(0)
 ; OTHER INFORMATION: Polypeptide Accession Number Q93074
 ; US-09-538-092-1377

Query Match 14.0%; Score 201; DB 4; Length 2124;
 Best Local Similarity 29.2%; Pred. No. 8,6e-10;
 Matches 87; Conservative 15; Mismatches 90; Indels 106; Gaps 11;
 QY 7 QLOPQNPSSQCPQEQVPLVQQQFPQQ--QCPFPQCPY----- 43

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Page 7

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Job time : 20 secs

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Page 1

satisfying chosen parameters: 1585576

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- 7: /cgn2_6/p1odaae1.1/pubpa/US08_NEW_PUB.dep.*
- 8: /cgn2_6/p1odaae1.1/pubpa/US08_PUBCOMB.dep.*
- 9: /cgn2_6/p1odaae1.1/pubpa/US09_PUBCOMB.dep.*
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- 11: /cgn2_6/p1odaae1.1/pubpa/US09_NEW_PUB.dep.*
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- 15: /cgn2_6/p1odaae1.1/pubpa/US10_PUBCOMB.dep.*
- 16: /cgn2_6/p1odaae1.1/pubpa/US10_PUBCOMB.dep.*
- 17: /cgn2_6/p1odaae1.1/pubpa/US11_NEW_PUB.dep.*
- 18: /cgn2_6/p1odaae1.1/pubpa/US11_NEW_PUB.dep.*
- 19: /cgn2_6/p1odaae1.1/pubpa/US60_PUBCOMB.dep.*
- 20: /cgn2_6/p1odaae1.1/pubpa/US60_PUBCOMB.dep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query No.	Match Length	DB	ID	Description
1	1344.5	93.8	287	17	US-10-739-930-9777	Sequence 9777, Ap
2	1243.5	86.7	319	17	US-10-739-930-9619	Sequence 9619, Ap
3	1240	86.5	298	17	US-10-739-930-9770	Sequence 9770, Ap
4	589	41.1	327	17	US-10-739-930-9623	Sequence 9623, Ap
5	557.5	38.9	282	17	US-10-474-955-101	Sequence 101, App
6	546.5	38.1	298	17	US-10-739-930-9621	Sequence 9621, App
7	524	36.5	279	17	US-10-474-955-97	Sequence 97, Appl
8	524	36.5	279	17	US-10-474-955-99	Sequence 99, Appl
			279	17	US-10-474-955-98	Sequence 98, Appl
					US-10-474-955-100	Sequence 100, Appl

14	277	19.3	541	17	US-10-425-115-20091
15	274	19.1	283	17	US-10-425-115-20099
16	286	18.7	1162	11	US-09-884-773-2
17	288	18.1	1162	14	US-10-284-804-2
18	265.5	18.5	1063	14	US-10-161-927-54
19	265.5	18.1	905	16	US-10-431-4678-64
20	266	17.9	933	16	US-10-423-114-44003
21	247.5	17.3	390	15	US-10-434-599-27045
22	244.5	17.1	229	15	US-10-425-114-41056
23	230	16.7	358	14	US-10-104-047-3710
24	232.5	16.2	192	12	US-10-445-114-52411
25	231.5	16.1	148	14	US-10-425-117-15
26	230	16.0	1044	15	US-10-445-114-72709
27	229.5	15.8	362	17	US-10-425-115-26123
28	226	15.5	738	14	US-10-451-1678-238
29	225	15.7	1173	16	US-10-437-963-14474
30	225	15.7	1236	10	US-09-789-787-109
31	224.5	15.4	351	15	US-10-284-0459-2693
32	221	15.4	4952	15	US-10-051-874-56
33	221	15.4	5008	15	US-10-051-874-166
34	221	15.4	5159	15	US-10-085-198-112
35	221	15.4	5262	15	US-10-051-874-165
36	220.5	15.4	5262	15	US-10-051-874-165
37	220.5	15.4	5262	15	US-10-051-874-165
38	216.5	15.1	1024	16	US-10-283-829-19176
39	216.5	15.1	1153	16	US-10-419-446-12
40	215.5	15.0	1351	16	US-10-282-1223-7514
41	213.5	14.9	1359	15	US-10-437-963-19003
42	213	14.9	1362	9	US-10-282-1223-75656
43	213	14.9	1362	9	US-09-818-242-14009
44	211.5	14.7	1362	9	US-09-818-242-14009
45	208.5	14.5	1025	15	US-10-425-114-55600
46	208.5	14.5	1025	16	US-10-437-963-113311

ATTACHMENTS

Sequence 200100, A
Sequence 200099, A
Sequence 2, Appl1
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Sequence 54, Appl1
Sequence 64, Appl1
Sequence 44003, A
Sequence 270450, A
Sequence 41056, A
Sequence 5710, Ap
Sequence 52411, A
Sequence 15, Appl1
Sequence 72709, A
Sequence 261231, A
Sequence 26123, A
Sequence 263, Ap
Sequence 144743, A
Sequence 10079, Ap
Sequence 2633, Ap
Sequence 5653, Ap
Sequence 116, Ap
Sequence 115, Ap
Sequence 165, Ap
Sequence 167, Ap
Sequence 176, Ap
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Sequence 190032, A
Sequence 75965, A
Sequence 14009, A
Sequence 55600, A
Sequence 11916, A

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Query Match	93.6%	Score 1344.5;	DB 17;	Length 287;
Best Local Similarity	95.1%	Pred. No. 6e-98;		
Matches 254; Conservative	0;	Mismatches 12;	Indels 1;	Gaps 1;

[illegible]


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; Sequence 101, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan W.
; APPLICANT: Konig, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: DO BINDING PROLAMINE-DERIVED PEPTIDES
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of GAMMA-1
US-10-474-955-101

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Query Match      38.9%; Score 557.5; DB 17; Length 282;
Best Local Similarity 47.6%; Pred. No. 5.5e-36;
Matches 138; Conservative 32; Mismatches 73; Indels 47; Gaps 15;

QY 2 RVPVYQQL-----QPNPSQQQPEQVPLVQQQCFPGQ-QQQF-----PQQPYPPQ-QPPPS 51
DB 10 QVPHQQQPFQPPHPPSQPPQPPQPPQPPQPPHQQPPQPPSQPPQPPQPPQPPQPPQPPQPPQ 68
QY 52 --QQPYLQ--LQPPPPHLP-YPQPPSPFPQPPYPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 106
DB 69 QPQPPYPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 118
QY 107 QQQQQQQQLLQQQLLQPCMDVVLQCHN-----IAHARSQVLAQSTYQLLQELCCQHLMQ 162
DB 119 PQQQPPSLIQSLQQQLLPCNKFLLQCKPVSLSLSMSLILPSSDCQVWQCCQQLAQ 178
QY 163 IPEQSQCCAIHNVVAIILHQQQKQQQPPSSQVSPQPL-QQYPLGGGSRFPQQNPQAQ 221
DB 179 IPQQAQCAIHSIVASIIHQEQGEQPPQ---GVQLIVPLSSQQQVGGQTL-----VQGGQ 229

QY 222 GSVQPPQQLPQPEEIRNLALQTLIPAMCNVYIAPYCTI--APF-----GIFG 264
DB 230 GIQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 279

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RESULT 6
US-10-739-930-9621
; Sequence 9621, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 9621
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIA-23APR03-C125-65-J
US-10-739-930-9621

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Query Match      38.1%; Score 546.5; DB 17; Length 298;
Best Local Similarity 46.9%; Pred. No. 4.3e-35;
Matches 134; Conservative 26; Mismatches 75; Indels 49; Gaps 14;

QY 4 PVPQQLPQNPSSQQQPEQVPLVQQQCFPGQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 61

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DB 36 PVP--QPHQPPSQQP-----QQTFFPQQTFFPHQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 84
QY 62 P-QPHLPYPPQPPSPFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 110
DB 85 PQQPPQPPFPQ-----QPPQPPFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 140
QY 111 QQQILQQQLLQQQLLQPCMDVVLQCHN-----IAHARSQVLAQSTYQLLQELCCQHLMQIPBQ 166
DB 141 QPPFIPSPHQQVNPCKRFFLLQCKPVSLSLSMSIMIPQSDQVWRQCCQQLAQIPQ 200
QY 167 SQCCAIHNVVAIILHQQQKQQQPPSSQVSPQPL-QQYPLGGGSRFPQQNPQAQGSVQ 225
DB 201 LQCCAIHTIHSIILHQQEQSQQQ---GWHILPLVQQQVGGQTL-----VQGGQITQ 251

QY 226 PQQLPQPEEIRNLALQTLIPAMCNVYIAPYCTI--APF-----GIFG 264
DB 252 PQQPAQLXAIRSLVLQTLPTMCNVYVPPESCIKAFSSVVAIGG 297

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RESULT 7
US-10-474-955-97
; Sequence 97, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan W.
; APPLICANT: Konig, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solliid Magne
; TITLE OF INVENTION: DO BINDING PROLAMINE-DERIVED PEPTIDES
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid sequence
US-10-474-955-97

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Query Match      36.5%; Score 524; DB 17; Length 279;
Best Local Similarity 46.2%; Pred. No. 2.4e-33;
Matches 132; Conservative 26; Mismatches 76; Indels 52; Gaps 14;

QY 4 PVPQQLPQNPSSQQQPEQVPLVQQQCFPGQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 61
DB 18 PVP--QPHQPPSQQP-----QQTFFPQQTFFPHQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 66
QY 62 P-QPHLPYPPQPPSPFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 110
DB 67 PQQPPQPPFPQ-----QPPQPPFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 122
QY 111 QQQILQQQLLQQQLLQPCMDVVLQCHN-----IAHARSQVLAQSTYQLLQELCCQHLMQIPBQ 166
DB 123 QPPFIPSPHQQVNPCKRFFLLQCKPVSLSLSMSIMIPQSDQVWRQCCQQLAQIPQ 182
QY 167 SQCCAIHNVVAIILHQQQKQQQPPSSQVSPQPL-QQYPLGGGSRFPQQNPQAQGSVQ 225
DB 183 LQCCAIHTIHSIILHQQEQSQQQ---GWHILPLVQQQVGGQTL-----VQGGQITQ 230

QY 226 PQQLPQPEEIRNLALQTLIPAMCNVYIAPYCTI--APF-----GIFG 264
DB 231 PQQPAQLXAIRSLVLQTLPTMCNVYVPPESCIKAFSSVVAIGG 276

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RESULT 8
US-10-474-955-99
; Sequence 99, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:

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Query Match 36.3% Score 520; DB 17; Length 279;
Best Local Similarity 45.8%; Pred. No. 4.9e-33;
Matches 131; Conservative 26; Mismatches 77; Indels 52; Gaps 14.

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Query Match: 36.3%; Score 520; DB 17; Length 279;
Best Local Similarity: 46.0%; Pred. No. 4, 9e-33;
Matches 131; Conservative 28; Mismatches 76; Indels 50; Gaps 14

QY      4  PYNQLPQNPSCQQPQDEQVYLYQQQQPFGCQQQQGP--PQDEYQRPQRPFSQQRPLYLQLQRF 61
Db      18  PVP--QRPQPSQSP-----QQTFPQQRQTFRHNRQQQFQRPQQ--PQQQFLQPSQSP 66

QY      62  P-QPHLFYQ-----PQSFRQQRYP---QRPQSYQRPQRPISQQQAQQQQQQQQQQQQ 111
Db      67  PQPQRPQYRPQRPQQLFQYQYQQLFQPSQQRQQQSFQSQQQYFQ---PQRPQSFQQQ 123

QY      112  QQQLQQQLPQQQLPCMDVYLQQHN-----IAHRSQVLYQQSTYQLDLCLCCQHLMOJPEQS 167
Db      124  PRPIQPSLQQQVMPKCNFLPQQCKYSLVLSLMSKIMIPQSDQCYVMRQSSQQLAQIPQQL 183

QY      168  QCCAIHNVVHAIIILHQQKQKQQQSSQVQSFQRP--QYPLQGSFRSQQNPPAQSSVQR 226
Db      184  QCAIHITVHHSIMQDEQQ-----GNIHLLPYQQQOVGQQGL-----VQGGGIIQP 231

QY      227  QQLPQFEELRNLLQTLPMQCNVYIAPYCTI--APF-----GIQG 264
Db      232  QQPAQLAIRSLVQLTLPQCNVYVPECSIIKAPFSQSVAGIIG 276

RESULT 11
US-10-739-930-9778
; Sequence: 9778, Application US/10739930
; Publication No. US20040216190A1

```


SEQ ID NO 200100
LENGTH: 541
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(541)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_114080C.1.pep
US-10-425-115-200100

Query Match 19.3%; Score 277; DB 17; Length 541;
Best Local Similarity 37.5%; Pred. No. 1.4e-13;
Matches 90; Conservative 20; Mismatches 80; Indels 50; Gaps 11;

QY 9 QPQNPSSQVQPEVPLVQQQPPGQQQPPFPQPPYPPQPPPSQPPYLQPPFPQPHLPY 68
DB 328 KPQASTQPTMQQ---QQLQQPQQQQQQQL-QQHFMPPQGLPLQDSQWQLQ-----Q 375
QY 69 POPSPPQQPYV---QPQPYQSPQ-QPISQQQAQQQQQQQQQQQQQQQQQQQQQLLQQLLQQQL 124
DB 376 QPQPMQPMQQQQPSQMQQQQMSMQQQMPMQQQMQHQQQQQMQQQQQQQQQQQQQQQQ 433
QY 125 PCMDVVLQQHNIAHANSQVLOQSTYQLQLQLCCGLMQLPESQCCQALHNVAIILHQ 184
DB 434 -----QQQQQQQLPQQQQQQQQQQQQQQQQQQQQ-----QPQQQQQQM-----QQ 470
QY 185 QKQGGQSSQVSSQPPQLQVPLQGSFRP-SQONPQAQSVQPPQLPQPEEIRNLALQT 243
DB 471 QQQQMQPQ-----QQQMQMQQQQQQQQQPQQQQQPPMVGTMGQ---QTMGHNRAVQVM 522

RESULT 15

US-10-425-115-200097
Sequence 200097, Application US/10425115
Publication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 200097
LENGTH: 283
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(283)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_114078C.1.pep
US-10-425-115-200097

Query Match 19.1%; Score 274; DB 17; Length 283;
Best Local Similarity 38.2%; Pred. No. 1.2e-13;
Matches 92; Conservative 20; Mismatches 71; Indels 58; Gaps 13;

QY 9 QPQNPSSQVQPEVPLVQQQPPGQQQPPFPQPPYPPQPPPSQPPYLQPPFPQPHLPY 68
DB 76 KPQASTQPTMQQ---QQLQQPQQQQQQQL-QQHFMPPQGLPLQDSQWQLQ-----Q 123
QY 69 POPSPPQQPYV---QPQPYQSPQ-QPISQQ-QAQQQQQQQQQQQQQQQQQQQQQLLQQLLQQQL 123
DB 124 QPQPMQPMQQQQPSQMQQQQMSMQQQMPMQQQMQHQQQQQMQQQQQQQQQQQQQQQQ 183
QY 125 PCMDVVLQQHNIAHANSQVLOQSTYQLQLQLCCGLMQLPESQCCQALHNVAIILHQ 183

DB 184 QP-----QQQQM-----QQMQQQQQQQMQ-----PQQQQMQM-----Q 211
QY 184 QKQGGQSSQVSSQPPQLQVPLQGSFRP-SQONPQAQSVQPPQLPQPEEIRNLALQT 242
DB 212 QQQQQMQPQ-----QQQMQMQQQQQQQMQPQQQQQPPMVGTMGQ---QPMGHNRAVQVM 263
QY 243 L 243
DB 264 M 264

Search completed: December 14, 2004, 17:35:34
Job time : 66.8333 secs

1	1363	95.0	286	2	S07923	alpha/beta-gliadin
2	1355	94.5	286	1	EMW4	alpha/beta-gliadin
3	1311	91.4	288	2	T06282	alpha-gliadin prec
4	1265.5	88.3	291	2	T06498	alpha/beta-gliadin
5	1266.5	88.3	307	2	S10015	alpha/beta-gliadin
6	1262	88.0	296	2	S07261	alpha/beta-gliadin
7	1260	87.9	313	2	S07924	alpha/beta-gliadin
8	1256	87.6	296	2	A27319	gliadin - wheat
9	1247.5	87.0	319	2	A23264	alpha/beta-gliadin
10	1244.5	86.8	319	2	C22364	alpha/beta-gliadin
11	1234.5	85.1	297	2	T06500	alpha/beta-gliadin
12	1222	85.2	326	2	D22364	alpha/beta-gliadin
13	1205	84.0	320	2	E22364	alpha/beta-gliadin
14	1182	82.4	282	2	T06504	alpha/beta-gliadin
15	1154.5	80.5	292	2	B22364	alpha/beta-gliadin
16	588	41.0	327	2	JS0402	gamma-gliadin prec
17	548.5	38.2	291	1	EMW3	gamma-gliadin B pr
18	540	37.7	302	2	JA0153	gamma-gliadin prec
19	488	34.0	305	2	S08312	gamma-bordein 1 pr
20	468	32.6	286	2	T05718	gamma-bordein 3 -
21	460.5	32.1	374	2	T05923	glutenin low molec
22	456.5	31.8	359	2	T06982	glutenin low molec
23	453.5	31.6	356	2	S01992	glutenin low molec
24	447.5	31.2	304	2	T06505	glutenin B1 - barley
25	446	31.1	293	2	S07365	glutenin (clone
26	445	31.0	264	2	S07975	B3-bordein)
27	442	30.8	285	2	S20853	glutenin low molec
28	442	30.8	286	2	T05920	glutenin low molec
29	441.5	30.8	298	2	T06980	glutenin low molec

30	440	30.7	303	2	T06961	low-molecular-weight
31	439.5	30.6	307	2	S04335	glutinin B low molec
32	438.5	30.6	290	2	S00519	hordein B precursor
33	427	29.8	251	2	P50034	gamma-gliadin prec
34	425.5	29.7	271	2	T04474	B1 hordein - barley
35	416	29.0	295	1	U00656	glutelin low molec
36	410.5	28.6	209	2	B64433	avenin precursor -
37	407	28.4	220	2	J01046	avenin precursor (
38	390.5	27.2	194	2	A23277	gamma-secalin - ry
39	385	26.8	243	2	S07976	B1-hordein (clone
40	383	26.7	244	2	S07398	gamma-gliadin B pr
41	382.5	26.7	222	2	J01047	avenin precursor (
42	379.5	26.5	323	2	T06506	glutelin low molec
43	376	26.2	182	2	JG0015	avenin N9 - oat
44	376	26.2	261	2	S57655	glutelin low molec
45	367.5	25.6	276	2	S57656	glutelin low molec

S07923
alpha/beta-gliadin precursor - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 20-Aug-1999
C:Accession: S07923
R:Sumner-Smith, M.; Rafalski, J.A.; Sugiyama, T.; Stoll, M.; Soell, D.
N:Critical Acids Res. 13, 3905-3916, 1985
A:Title: Conservation and variability of wheat alpha/beta-gliadin genes.
A:Reference numbers: S07361, MUID:55242077, PMID:3893304
A:Accession: S07923
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-286 <STUD>
A:Cross-references: EMBL:X02539; NID:G21760; PIDN:CAA6384.1; PID:G21761
C:Superfamily: gliadin

Query Match	95.0%	Score 1363;	DB 2;	Length 286;
Best Local Similarity	95.9%	Pred No.2.5e-84;		
Matches 255;	Conservative	0;	Mismatches 11;	Indels 0;
				Gaps 0;

alpha/beta-gliadin precursor - wheat
N/Alternate names: prolamins
C/Species: Triticum aestivum (common wheat)
C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C/accession: A03354
R/rafielski, J.A.; Scheets, K.; Metzler, M.; Peterson, D.M.; Hedgcock, C.; Solli, D.G.
EMBO J. 3, 1409-1415, 1984
A./title: Developmentally regulated plant genes: the nucleotide sequence of a wheat gl

D22364
 alpha/beta-gliadin precursor (clone A735) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: D22364
 R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
 J. Biol. Chem. 260, 8203-8213, 1985
 A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
 A/Reference number: A92541; MUID:85234522; PMID:2989281
 A/Accession: D22364
 A/Molecule type: mRNA
 A/Residues: 1-326 <OKI>
 A/Cross-references: UNIPROT:P04724
 C/Superfamily: gliadin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-326/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 85.2%; Score 1222; DB 2; Length 326;
 Best Local Similarity 77.8%; Pred. No. 7.3e-75;
 Matches 238; Conservative 9; Mismatches 19; Indels 40; Gaps 4;

QY 1 VRVPVPLQPNPNSQQQPEQVPLVQQQCFPGQQQFPFPQPPYQPPFPFSQQPYLQ 60
 DB 21 VRVPVPLQPNPNSQQQPEQVPLVQQQCFPGQQQFPFPQPPYQPPFPFSQQPYLQ 80
 QY 61 F-----PQPHLPYQPSFPFPQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQ 107
 DB 81 FPPQPPFPFPQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQ 140
 QY 108 QQQQQQILQQILQQQLIPCDVVLQCHNIAHARSQVLAQSTYQLQELCCQHLMOLEPES 167
 DB 141 QQQQQQILQQILQQQLIPCDVVLQCHNIAHARSQVLAQSTYQLQELCCQHLMOLEPES 200
 QY 168 QQQAHNVVHAIIH-----QQQKQQQSSQVSYQQPLQ 202
 DB 201 RCQAHNVVHAIIHQQQQQQEQKQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 260
 QY 203 QYPLQGSFRPQQNPQAQGSVPQQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPF 260
 DB 261 QYPSGGSFQPSQQNPQAQGSVPQQLPQFEIRNLALQTLPAKCNVYIIPYCTTIAPY 320
 QY 261 GTFGTN 266
 DB 321 GTFGTN 326

RESULT 13
 B22364
 alpha/beta-gliadin precursor (clone A1235) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: E22364
 R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
 J. Biol. Chem. 260, 8203-8213, 1985
 A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
 A/Reference number: A92541; MUID:85234522; PMID:2989281
 A/Accession: E22364
 A/Molecule type: mRNA
 A/Residues: 1-320 <OKI>
 A/Cross-references: UNIPROT:P04723
 C/Superfamily: gliadin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-320/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 84.0%; Score 1205; DB 2; Length 320;
 Best Local Similarity 79.0%; Pred. No. 9.8e-74;
 Matches 237; Conservative 11; Mismatches 18; Indels 34; Gaps 5;

QY 1 VRVPVPLQPNPNSQQQPEQVPLVQQQCFPGQQQFPFPQPPYQPPFPFSQQPYLQ 59
 DB 21 VRVPVPLQPNPNSQQQPEQVPLVQQQCFPGQQQFPFPQPPYQPPFPFSQQPYLQ 80
 QY 60 PFPQ-----PFLPYPQPSFPFPQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQ 113

DB 81 PFPQPPFPFPQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQ 140
 QY 114 ILQQLILQQILIPCDVVLQCHNIAHARSQVLAQSTYQLQELCCQHLMOLEPESQQA 173
 DB 141 TLQQLILQQILIPCDVVLQCHNIAHARSQVLAQSTYQLQELCCQHLMOLEPESQQA 200
 QY 174 NVVHAIIH-----QQQKQQQSSQVSYQQPLQ 208
 DB 201 NVVHAIIHQQQQQQEQKQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 260
 QY 203 GSTRPQQNPQAQGSVPQQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPF 266
 DB 261 VSTRPQQNPQAQGSVPQQLPQFEIRNLALQTLPAKCNVYIIPYCTTIAPF 320

RESULT 14
 T06504
 alpha/beta-gliadin precursor (A-III) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T06504
 R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
 J. Biol. Chem. 260, 8203-8213, 1985
 A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
 A/Reference number: A92541; MUID:85234522; PMID:2989281
 A/Accession: T06504
 A/Molecule type: preliminary; translated from GB/EMBL/DBJ
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 1-282 <OKI>
 A/Cross-references: UNIPROT:P04723; EMBL:M1076; NID:G170725; PIDN:AAA4283.1; PID:G17
 C/Superfamily: gliadin
 C/Keywords: seed; storage protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-282/Product: alpha/beta-gliadin A-III #status predicted <MAT>

Query Match 82.4%; Score 1182; DB 2; Length 282;
 Best Local Similarity 84.8%; Pred. No. 3e-72;
 Matches 228; Conservative 11; Mismatches 20; Indels 10; Gaps 4;

QY 1 VRVPVPLQPNPNSQQQPEQVPLVQQQCFPGQQQFPFPQPPYQPPFPFSQQPYLQ 59
 DB 21 VRVPVPLQPNPNSQQQPEQVPLVQQQCFPGQQQFPFPQPPYQPPFPFSQQPYLQ 80
 QY 60 PFPQPPFPFPQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQ 119
 DB 81 PFPQPPFPFPQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQPPYQ 133
 QY 120 QQLILPQMDVVLQCHNIAHARSQVLAQSTYQLQELCCQHLMOLEPESQQA 179
 DB 134 QQLILPQMDVVLQCHNIAHARSQVLAQSTYQLQELCCQHLMOLEPESQQA 193
 QY 160 ILHQKQQQQQSSQVSYQQPLQYPLQSGSFRPQQNPQAQGSVPQQLPQFEIRNL 239
 DB 194 ILHQKQQQQQSSQVSYQQPLQYPLQSGSFRPQQNPQAQGSVPQQLPQFEIRNL 253
 QY 240 LQTLPAKCNVYIAPYC--TIAPF 266
 DB 254 LQTLPAKCNVYIIPYCTTIAPF 320

RESULT 15
 B22364
 alpha/beta-gliadin precursor (clone A26) - wheat
 C/Species: Triticum aestivum (common wheat)
 C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C/Accession: E22364
 R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
 J. Biol. Chem. 260, 8203-8213, 1985
 A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
 A/Reference number: A92541; MUID:85234522; PMID:2989281
 A/Accession: E22364
 A/Molecule type: mRNA

A:Residues: 1-292 <OK>

A:Cross-references: UNIPROT:P04721

C:Superfamily: gliadin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-292/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 80.5%; Score 1154.5; DB 2; Length 292;

Best Local Similarity 84.1%; Pred. No. 2.1e-70; Indels 31; Gaps 4;

Matches 227; Conservative 2; Mismatches 10;

```

1 VRVVPQLQPNPSQQQPEQVPLVQQQPFPGQQQPPPPQPPPPQPPPPSQQPYLQLQP 60
21 VRVVPQLQLQNPSSQQPEQVPLVQQQFLGQQQPPPPQPPPPQPPPPSQQPYLQLQP 80
61 F--PQ--PHLPYPPQSFPPQPPYPPQPPYSPQPPIS--QQQAQQQQQQQQQQQQQQQ 114
81 FLQPQPPPPPLPYSQPFPFPQPPYPPQPPYSPQPPISQQQQQQQQQQQQQQQQQQQ 140
115 LQQLLQQLIPCMQVVLQCHNTAHASQVLAQSTYQLLQELCCQHLWQIPRQSCCAIHN 174
141 IQQLLQQLIPCMQVVLQCHNTVHKSQVLAQSTYQLLQELCCQHLWQIPRQSCCAIHN 200
175 VVAHIIILH-----QQQKQQQPSQSQSFQQPLQGYPLGQG 209
201 VVAHIIILHQQCCQQQEQKQQLQQQQQQQQQQQQQQQQKQQQPSQSQSFQQPLQGYPLGQG 260
210 SFRSQQNPQAQGSVPQQLPQFEIRNLA 239
261 SFRSQQNPQAQGSVPQQLPQFEIRNLA 290
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Search completed: December 14, 2004, 17:26:59
Job time: 16 secs

RESULT 4

Q92P09 PRELIMINARY; PRT; 288 AA.
 AC Q92P09
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-gliadin precursor (Fragmenc).
 GN Name=alpha-gliadin;
 OS Triticum aestivum subsp. spelta.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 NCBI_TaxId=56933;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Kasarda D.D., D'Ovidio R.;
 RT "deduced amino acid sequence of an alpha-gliadin gene from Spelt wheat
 (Spelta) includes sequences active in celiac disease.";
 RL Cereal Chem. 76:548-551(1999).
 DR EMBL; AJ130948; CAB10257.1; -
 DR PIR; S13333; S13333.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gliadin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR SMART; SM00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 KW Signal.
 FT SIGNAL 1 20 Potential.
 FT CHAIN 21 >288 alpha-gliadin.
 FT NON_TER 288 288
 SQ SEQUENCE 288 AA; 33203 MW; DA058F3FAFA6B6C6 CRC64;

Query Match 94.4%; Score 1353; DB 2; Length 288;
 Best Local Similarity 95.1%; Pred. No. 1e-74;
 Matches 255; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

QY 1 VEVVPVQLQPNPNSQQQPEQVPLVQQQPFPGQQQFPFQQQPYFPQPFPSQQPYLQLQP 60
 DB 21 VEVVPVQLQPNPNSQQQPEQVPLVQQQPFPGQQQFPFQQQPYFPQPFPSQQPYLQLQP 80
 QY 61 FPOPHLPYRQPSFPPQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQ 118
 DB 81 FPOPHLPYRQPSFPPQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQ 140
 QY 119 LQQQLIPCMQVVLQCHNIAHARSQYLQOSTYQLLQELCCQHLWQIPQSQCCQAIHNV 178
 DB 141 LQQQLIPCMQVVLQCHNIAHARSQYLQOSTYQLLQELCCQHLWQIPQSQCCQAIHNV 200
 QY 179 ILLHQOQKQOQSSQVSPQQLQCYRIGGSGFRPSQCNPPAQSGSVQPPQLPQFEETRL 238
 DB 201 ILLHQOQKQOQSSQVSPQQLQCYRIGGSGFRPSQCNPPAQSGSVQPPQLPQFEETRL 260
 QY 239 ALQTLPAMCNVYIAYCTIAPFGIFGTN 266
 DB 261 ALQTLPAMCNVYIAYCTIAPFGIFGTN 288

RESULT 5
 Q9M4M5 PRELIMINARY; PRT; 274 AA.
 AC Q9M4M5
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-gliadin.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.

OX NCBI_TaxId=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mjoelner; TISUS=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Solild L.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133603; CAB76955.1; -
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gliadin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 FT CHAIN 1 274 alpha-gliadin.
 SQ SEQUENCE 274 AA; 31980 MW; 976919397534ABD CRC64;

Query Match 94.1%; Score 1349.5; DB 2; Length 274;
 Best Local Similarity 94.1%; Pred. No. 1.6e-74;
 Matches 255; Conservative 0; Mismatches 11; Indels 5; Gaps 1;

QY 1 VEVVPVQLQPNPNSQQQPEQVPLVQQQPFPGQQQFPFQQQPYFPQPFPSQQPYLQLQP 60
 DB 2 VEVVPVQLQPNPNSQQQPEQVPLVQQQPFPGQQQFPFQQQPYFPQPFPSQQPYLQLQP 61
 QY 61 FPOPHLPYRQPSFPPQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQ 115
 DB 62 FPOPHLPYRQPSFPPQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQPYRQ 121
 QY 116 QQLIQQLIPCMQVVLQCHNIAHARSQYLQOSTYQLLQELCCQHLWQIPQSQCCQAIHNV 175
 DB 122 QQLIQQLIPCMQVVLQCHNIAHARSQYLQOSTYQLLQELCCQHLWQIPQSQCCQAIHNV 181
 QY 176 VHAITLHQOQKQOQSSQVSPQQLQCYRIGGSGFRPSQCNPPAQSGSVQPPQLPQFEET 235
 DB 182 VHAITLHQOQKQOQSSQVSPQQLQCYRIGGSGFRPSQCNPPAQSGSVQPPQLPQFEET 241
 QY 236 RNLALQTLPAMCNVYIAYCTIAPFGIFGTN 266
 DB 242 RNLALQTLPAMCNVYIAYCTIAPFGIFGTN 272

RESULT 6
 Q9M4M2 PRELIMINARY; PRT; 276 AA.
 AC Q9M4M2
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-gliadin.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 NCBI_TaxId=4565;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mjoelner; TISUS=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Solild L.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133606; CAB76958.1; -
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gliadin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 FT CHAIN 1 276 alpha-gliadin.

OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mjocelner; TISSUE=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Sollid L.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133608; CAB76960.1; -
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAT.
 DR InterPro; IPR001954; Glia_glutenin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR SMART; SM00499; AAT; 1.
 DR CHAIN 1
 FT SEQUENCE 276 AA; 32211 MW; 6A2B9723D42B100A CRC64;
 SQ
 Query Match 93.5%; Score 1340.5; DB 2; Length 276;
 Best Local Similarity 92.7%; Pred. No. 5.8e-74;
 Matches 253; Conservative 2; Mismatches 11; Indels 7; Gaps 1;
 QY 1 VRVVPOLQPNPSSQSQPQEQVPLVQCCQFPGQQQCFPPQOPYPQOPFPFSQCPYLQLP 60
 Db 2 VRVVPOLQPNPSSQSQPQEQVPLVQCCQFPGQQQCFPPQOPYPQOPFPFSQCPYLQLP 61
 QY 61 FPQPHLPYPOQSPFPQOPYPQOPQYSPQOPQPSQQAQQQQQQQQQQ-----QQ 113
 Db 62 FPQQLYSQPPFPQOPYPQOPQYSPQOPQPSQQAQQQQQQQQQQQQQQQQQQQEQ 121
 QY 114 ILQQLIQQLIPCHDVVLCQHNIHARSQVLCQSTYQLQLCCQHLWQIPESQCAIHW 173
 Db 122 ILQQLIQQLIPCHDVVLCQHNIHARSQVLCQSTYQLQLCCQHLWQIPESQCAIHW 181
 QY 174 NVVHAIIHQCKQKQSSQVSPFQPLQYPLQGSFRPSQNPQAQGSVPQQLPQFE 233
 Db 182 NVVHAIIHQCKQKQSSQVSPFQPLQYPLQGSFRPSQNPQAQGSVPQQLPQFE 241
 QY 234 EIRNLALQTLPMKCNVYIAPYCTIAPFGIFGTN 266
 Db 242 EIRNLALQTLPMKCNVYIAPYCTIAPFGIFGTN 274
 RESULT 10
 Q41531 PRELIMINARY; PRT; 289 AA.
 ID Q41531;
 AC Q41531;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Alpha-glialin storage protein.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cheyenne;
 RA Anderson O.D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U51306; AAA96524.1; -
 DR PIR; S13333; S13333.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAT.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Glia_glutenin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.

DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAT; 1.
 DR SEQUENCE 289 AA; 33349 MW; 5F577C9CD63874FA CRC64;
 SQ
 Query Match 93.2%; Score 1336.5; DB 2; Length 289;
 Best Local Similarity 94.1%; Pred. No. 1.1e-73;
 Matches 253; Conservative 1; Mismatches 12; Indels 3; Gaps 1;
 QY 1 VRVVPOLQPNPSSQSQPQEQVPLVQCCQFPGQQQCFPPQOPYPQOPFPFSQCPYLQLP 60
 Db 21 VRVVPOLQPNPSSQSQPQEQVPLVQCCQFPGQQQCFPPQOPYPQOPFPFSQCPYLQLP 80
 QY 61 FPQPHLPYPOQSPFPQOPYPQOPQYSPQOPQPSQQAQQQQQQQQQQ-----QQ 117
 Db 81 FPQPHLPYPOQSPFPQOPYPQOPQYSPQOPQPSQQAQQQQQQQQQQQQQQQQQQQ 140
 QY 118 ILQQLIQQLIPCHDVVLCQHNIHARSQVLCQSTYQLQLCCQHLWQIPESQCAIHWVH 177
 Db 141 ILQQLIQQLIPCHDVVLCQHNIHARSQVLCQSTYQLQLCCQHLWQIPESQCAIHWVH 200
 QY 178 AIIHQCKQKQSSQVSPFQPLQYPLQGSFRPSQNPQAQGSVPQQLPQFEIRN 237
 Db 201 AIIHQCKQKQSSQVSPFQPLQYPLQGSFRPSQNPQAQGSVPQQLPQFEIRN 260
 QY 238 LALQTLPMKCNVYIAPYCTIAPFGIFGTN 266
 Db 261 LALQTLPMKCNVYIAPYCTIAPFGIFGTN 289
 RESULT 11
 Q5M4L9 PRELIMINARY; PRT; 270 AA.
 ID Q5M4L9;
 AC Q5M4L9;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Alpha-glialin.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mjocelner; TISSUE=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Sollid L.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ133609; CAB76961.1; -
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAT.
 DR InterPro; IPR001954; Glia_glutenin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAT; 1.
 DR CHAIN 1
 FT SEQUENCE 270 AA; 31491 MW; 1DB4B6528EFAADF5 CRC64;
 SQ
 Query Match 92.7%; Score 1329.5; DB 2; Length 270;
 Best Local Similarity 94.0%; Pred. No. 2.6e-73;
 Matches 251; Conservative 3; Mismatches 12; Indels 1; Gaps 1;
 QY 1 VRVVPOLQPNPSSQSQPQEQVPLVQCCQFPGQQQCFPPQOPYPQOPFPFSQCPYLQLP 60
 Db 2 VRVVPOLQPNPSSQSQPQEQVPLVQCCQFPGQQQCFPPQOPYPQOPFPFSQCPYLQLP 61
 QY 61 FPQPHLPYPOQSPFPQOPYPQOPQYSPQOPQPSQQAQQQQQQQQQQ-----QQ 119
 Db 62 FPQPHLPYPOQSPFPQOPYPQOPQYSPQOPQPSQQAQQQQQQQQQQQQQQQQQQQ 121

DR EMBL; U51304; AAA96523.1; -.
 DR PIR; S13333; S13333.
 DR PIR; T06282; T06282.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gliadin.
 DR Pfam; PF00234; Tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SMO0499; AAI; 1.
 DR SEQUENCE 288 AA; 33285 MW; D7F6E9133283CA2 CRC64;

Query Match 91.4%; Score 1311; DB 2; Length 288;
 Best Local Similarity 92.5%; Pred. No. 3.7e-72;
 Matches 248; Conservative 3; Mismatches 15; Indels 2; Gaps 1;

QY 1 VRVFPVQLQPNBSCQQLFQEQVPLVQQQQLFGQQQFPFPQGPYPQQLFSPQLYLQLP 60
 DB 21 VRVFPVQLQPNBSCQQLFQEQVPLVQQQQLFGQQQFPFPQGPYPQQLFSPQLYLQLP 80
 QY 61 FPQPHLPYPQPSFPQGPYPQGPQYSPQGPISQQAQQQQQQQQQQQQ--QQILQQI 118
 DB 81 FSPQLPYSPQGPFPQGPYPQGPQYSPQGPISQQAQQQQQQQQQQQQ--QQILQQI 140
 QY 119 LQQQLPCMDVYLQHNIAHARSQVLAQSTYQLQLQELCCQHLWQIPBOSQCAIHNVYHA 178
 DB 141 LQQQLPCMDVYLQHNIAHARSQVLAQSTYQLQLQELCCQHLWQIPBOSQCAIHNVYHA 200
 QY 179 ILHQQKQKQQQSSQVSPQQLQYPLQGSFRRSQQNPQAQSVQVQQLPQFEERINL 238
 DB 201 ILHQQKQKQQQSSQVSPQQLQYPLQGSFRRSQQNPQAQSVQVQQLPQFEERINL 260
 QY 239 ALQTLPMCNVYIAPYCTIAFPFGIFGTN 266
 DB 261 ALQTLPMCNVYIAPYCTIAFPFGIFGTN 288

RESULT 15
 Q41528
 ID Q41528 PRELIMINARY; PRT; 287 AA.
 AC Q41528;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Alpha-gliadin.
 OS Triticum aestivum (wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cheyenne;
 RA Anderson O.D.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50984; AAA96276.1; -.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gliadin.
 DR Pfam; PF00234; Tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SMO0499; AAI; 1.
 DR SEQUENCE 287 AA; 33193 MW; 05F82296749C9E97 CRC64;

Query Match 90.6%; Score 1298.5; DB 2; Length 287;
 Best Local Similarity 92.9%; Pred. No. 2.1e-71;
 Matches 249; Conservative 2; Mismatches 14; Indels 3; Gaps 3;

QY 1 VRVFPVQLQPNBSCQQLFQEQVPLVQQQQLFGQQQFPFPQGPYPQQLFSPQLYLQLP 60
 |||

DB 21 VRVFPVQLQPNBSCQQLFQEQVPLVQQQQLFGQQQFPFPQGPYPQQLFSPQLYLQLP 79
 QY 61 FPQPHLPYPQPSFPQGPYPQGPQYSPQGPISQQAQQQQQQQQQQ--QQILQQI 118
 DB 80 FPQPHLPYPQPSFPQGPYPQGPQYSPQGPISQQAQQQQQQQQQQ--QQILQQI 139
 QY 120 QQQQLPCMDVYLQHNIAHARSQVLAQSTYQLQLQELCCQHLWQIPBOSQCAIHNVYHA 179
 DB 140 QQQQLPCMDVYLQHNIAHARSQVLAQSTYQLQLQELCCQHLWQIPBOSQCAIHNVYHA 199
 QY 180 ILHQQKQKQQQSSQVSPQQLQYPLQGSFRRSQQNPQAQSVQVQQLPQFEERINL 238
 DB 200 ILHQQKQKQQQSSQVSPQQLQYPLQGSFRRSQQNPQAQSVQVQQLPQFEERINL 259
 QY 239 ALQTLPMCNVYIAPYCTIAFPFGIFGTN 266
 DB 260 ALQTLPMCNVYIAPYCTIAFPFGIFGTN 287

Search completed: December 14, 2004, 17:25:21
 Job time : 80 secs

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OM protein - protein search, using sw model

Run on: December 14, 2004, 17:00:05 ; Search time 76.6667 Seconds
(without alignments)
1244.635 Million cell updates/sec

Title:	US-10-089-700-3-K65
Perfect score:	1431
Sequence:	1 VRVPVQLQPNPSQQQPE.....CNVIAPYCTIAPFGIGTN 266

Scoring table: BLOSUM62

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Database : _A_Genseqrp23Sep04:*
1: Genseqrp1980s:*
2: Genseqrp1990s:*
3: Genseqrp2000s:*
4: Genseqrp2001s:*
5: Genseqrp2002s:*
6: Genseqrp2003as:*
7: Genseqrp2003bs:*
8: Genseqrp2004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Query Length	DB	ID	Description
No.						
1	1427	99.7	266	4	AAU01799	Aau01799 Wheat A-g
2	1427	99.7	266	8	ADH14513	Adh14513 A-glutadin
3	1267.5	88.6	290	7	AAE38874	Aae38874 Wheat alp
4	1267.5	88.6	290	8	ADP19626	Adp19626 Alpha-2-g
5	464	32.4	369	2	AAW62647	Aaw62647 Mature du
6	450.5	31.5	297	7	AD071669	Ado71669 Amino aci
7	440.5	30.8	307	7	ADH99338	Adh99338 T. aestiv
8	440.5	30.8	307	8	ADG44134	Adg44134 T. aestiv
9	437.5	30.6	298	8	AD071661	Ado71661 Amino aci
10	287.5	20.1	1798	4	ABH71695	Abh71695 Drosophil
11	271	18.9	2285	4	ABH63057	Abh63057 Drosophil
12	270	18.9	1162	3	AAV96255	Aav96255 Kaposi's
13	270	18.9	1162	3	AAV56500	Aav56500 HHV8 ORF
14	270	18.9	1162	4	AAH63621	Aah63621 Amino aci
15	270	18.9	1162	5	AAH05621	Aah05621 Kaposi's
16	270	18.9	1162	8	ADU65096	Adu65096 HHV8 late
17	266.5	18.6	757	8	ADCO3905	Adco3905 Human POL
18	266.5	18.6	1069	6	ABO07138	Ab007138 Novel hum
19	266.5	17.8	1069	8	ADJ37233	Adj37233 Human nuc
20	255	17.8	186	7	ADH99336	Adh99336 H. vulgar
21	255	17.8	186	8	ADG44132	Adg44132 H. vulgar
22	255	17.8	260	8	AD047673	Ado47673 Amino aci
23	251	17.5	905	5	ABG93053	Abg93053 S. cerev
24	251	17.5	905	6	ABR51130	Abri51130 Protein s
25	251	17.5	905	7	ADK62564	Adk62564 Disease t

26	250.5	17.5	900	4	ABB62018	Abb62018	Drosophila
27	242	16.9	1013	4	ABB71039	Abb71039	Drosophila
28	241	16.8	358	7	ABD65556	Abd65556	Human prot
29	238.5	16.7	1069	4	ABE61305	Abb61305	Drosophila
30	238.5	16.7	1442	7	ADC07868	Adc07868	Rice prot
31	234	16.4	4365	6	ABU02352	Abu02352	S. pneumoniae
32	233	16.3	160	7	ADH89335	Adh89335	H. vulgare
33	233	16.3	160	8	ADG44131	Adg44131	H. vulgare
34	231.5	16.2	149	4	ABG72673	Abg72673	Polydactylus
35	231	16.1	1761	4	ABE59512	Abd59512	Drosophila
36	231	16.1	2237	5	ABG70004	Abg70004	Larval val
37	231	16.1	2703	3	AAE54568	Hay54568	A. syntherisma
38	230	16.1	158	3	AAE60074	Abb60074	Drosophila
39	230	16.1	2880	4	ABE61650	Abb61650	Drosophila
40	227	15.9	738	5	ABG93140	Abb93140	S. cerevisiae
41	226	15.8	153	3	AAE69495	Hay69495	Amino acid
42	226	15.8	128	4	ABY70377	Abb70377	Drosophila
43	225.5	15.8	785	8	ADP98883	Adp98883	C. albicans
44	225	15.7	368	4	ABE63167	Abb63167	Drosophila
45	224	15.7	1337	3	AAE81609	Hay81609	Streptococcus

ALIGNMENTS

RESULT 1
AAU01799
ID AAU01799 standard; protein; 266 AA
XX:
AC AAU01799;

The sequence represents wheat A-gliadin A-gliadin derived peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can

The present invention describes a method (M1) for preventing or treating

XX	Treating celiac sprue and/or dermatitis herpetiformis comprises
PT	administering to a patient a dose of a glucanase that attenuates gluten
PT	toxicity in the patient.
XX	
PS	Example 2; Fig 4; 69pp; English.
XX	
CC	The present invention relates to a method for treating celiac sprue
CC	and/or dermatitis herpetiformis. The method involves administering to a
CC	patient a dose of a glucanase that attenuates gluten toxicity in the
CC	patient. The method is also useful in treating a foodstuff to render the
CC	foodstuff less toxic to a celiac sprue patient. The present sequence is
CC	wheat alpha-2 gliadin protein used to illustrate the method of the
CC	invention
XX	
SQ	Sequence 290 AA;
XX	
Query Match	88.6%; Score 1267.5; DB 7; Length 290;
Best Local Similarity	84.7%; Pred. No. 4,8e-101;
Matches 243; Conservative	9; Mismatches 14; Indels 21; Gaps 3
OY	
Db	1 VAVPVPOLQPQNPSSQQQPEQGVPLVQOQQCFPGQQQCFPPQCPYPQPFPPSQPYLQLQP 60
	2 VAVPVPOLQPQNPSSQQQPEQGVPLVQOQQCFPGQQCFPPQCPYPQPFPPSQPYLQLQP 61
OY	61 F-----PQKLPYPQSPFPFPQPPYPQPOFQYSQPPISQQQAQQQQQQQ 105
Db	62 FPQPOLPYPQPLPYPQPLPYPQPPQPFPPQCPYQSQPYVSQPPQPISSQQQQQQQQQQQ 121
OY	106 --QQQQQQQQQILIQQLIFCMVVLAQHNIHAVRSQVLQSTYTQLQEQCCQLMQI 163
Db	122 QHQQQQQQQQILIQQLIFCRDVLVQSHIAIGSSCVLQOSTYLVLCCQQLMQI 181
OY	164 PQQSCOCALHNVAHIIHLA---QQQKQQQCPSQVSPFQCPLOQYPLGGSFPPSQGNFQ 219
Db	182 PQQSCQCALHNVAHIIHLQQQQQQQQQQQQQLSGVSPFQCPQOQVPSGGSFPQSQGNFQ 241
OY	220 AGGSVQPPQPLPQFEIRNLALQTLPAMCNVYIAPYCTIAPFGIFGTN 266
Db	242 AGGSVQPPQPLPQFEIRNLALETLPAMCNVYIIPYCTIAPVGIFGTN 288
XX	
RESULT 4	
ADP19626	ID ADP19626 standard; protein; 290 AA.
XX	
AC	ADP19626;
XX	
DT	26-AUG-2004 (first entry)
XX	
DE	Alpha-2-gliadin protein, SEQ ID 28.
XX	
KW	Gluten; Celiac Sprue; wheat; gliadin; alpha-2-gliadin.
XX	
OS	Triticum aestivum.
XX	
PN	WO2004045392-A2.
XX	
PD	03-JUN-2004.
XX	
PF	20-NOV-2003; 2003WO-US037434.
XX	
PR	20-NOV-2002; 2002US-0428033P.
XX	
PA	(STRD) UNIV DELAND STANFORD JUNIOR.
XX	
PI	Khosia C, Shan L;
XX	
DR	WPI; 2004-460460/43.
XX	
PT	New gluten oligopeptides, useful for diagnosing Celiac Sprue, in
PT	diagnostic assays for detecting antibodies against such oligopeptides, or
PT	for producing antibodies that bind specifically to such oligopeptides.

[illegible]

XX The present sequence represents the mature glutenin protein. The DNA
 CC sequence encoding this protein is isolated from the genomic DNA of
 CC Triticum durum L. The gene codes for a low-molecular-weight glutenin
 CC protein and can be used to produce transgenic durum wheat plants with
 CC better quality characteristics (no details given). (Updated on 25-MAR-
 CC 2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS
 CC field)

SC Sequence 369 AA;

Query Match 32.4%; Score 464; DB 2; Length 369;

Best Local Similarity 40.2%; Pred. No. 1.2e-31;
 Matches 134; Conservative 32; Mismatches 87; Indels 80; Gaps 14;

6 PQLQPNSQGP-----QEVPLVQGGQPPGQGGQPP--EQGPYGPQPP-----50
 38 PQGPQSGQGGQPPPLSGQGGQPPGSGQGGQPPVLPQGPSSQGLPPFSQGGQPP 97
 51 ---SQGPV-----QLGPFPQKLPYGPQSGFPQ-----PYGPQGGYSQ 89
 98 FSGQGGQPPVLPQGPSSQGGQPPGSGQGGQPPVLPQGPSSQGGQPPFSQ 157
 90 PQGPISQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQ 132
 158 QGGQPPVLPQGPSSQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 216
 133 QH-----NIAHRSQVLAQSTYQLLQELCCGHLMOIPRSGQCGAIVHVAIILHQQK 186
 217 QGSPFAMPSQSLARSGMQLQSSCHWQGGQGGQGGQGGQGGQGGQGGQGGQGG 274
 187 QGGQPSQGSVFPQPLQGYLGGSGFPSSQGNPQAGS-----VGPQLPQFEE 234
 275 QGVQSSIQVQGGQPPQ---LGGCVSQQPQGGQGGQGGQGGQGGQGGQGGQGGQ 331
 235 IENLAQLTLPAMCNVYIAPY--CTAPPGIFET 265
 332 MTSIALRTLPYCMNVMPLRYRTTRVPGV--GT 363

RESULT 6
 ID ADO71669 standard; protein; 297 AA.

XX ADO71669;

XX 12-AUG-2004 (first entry)

XX Amino acid sequence of a modified glutenin LMW subunit.

XX low molecular weight subunit; LMW subunit; glutenin;
 XX wheat cultivar Cheyenne; gliadin; flour; tablet; celiac disease;
 XX gluten intolerance.

XX Triticum sp.
 OS Synthetic.

XX EP1424342-A1.

XX 02-JUN-2004.

XX 27-NOV-2002; 2002EP-00026461.

XX 27-NOV-2002; 2002EP-00026461.

XX (BAKE-) BAKEMARK DEUT GMBH.
 XX (MONS-) MONSANTO AGRAR DEUT GMBH.
 XX (UNIF-) UNIFERN GMBH & CO KG.
 XX (PURA-) PURATOS NV.

XX Hinemann E, Wieser H, Stahl U;

XX MPI, 2004-402870/38.

DR N-PSDB; ADO71669.
 XX Novel nucleic acid comprising sequence encoding modified glutenin
 PT polypeptide, useful for preparing modified glutenin polypeptide as
 PT gliadin substitute in foodstuffs such as dough, pastries and waters.
 XX Claim 16; Fig 11; 43pp; English.

XX The present sequence represents a modified low molecular weight (LMW)
 CC subunit of glutenin. The wild type subunit is designated clone LMW6, and
 CC is isolated from wheat cultivar Cheyenne. The LMW6 polypeptide does not
 CC contain the allergenic epitope QQQPP, and shows some minor differences to
 CC published sequences. It therefore represents a new allele for LMW subunit
 CC genes. The LMW6 polypeptide was modified to produce modified glutenin
 CC polypeptides of the invention. In these modified polypeptides one or more
 CC cysteine residues responsible for intermolecular cross linking through
 CC disulfide bridges are deleted or substituted. The modified glutenin
 CC polypeptide is useful as a gliadin substitute. It is also useful in the
 CC preparation of foodstuffs, such as flour or for the preparation of
 CC pharmaceutical products, such as tablets, where the foodstuffs contain a
 CC considerably reduced amount of gliadin proteins or no gliadin proteins.
 CC Pharmaceutical compositions comprising the modified polypeptide of the
 CC invention are useful for treating patients suffering from celiac disease
 CC or persons who are intolerant to gluten.

SC Sequence 297 AA;

Query Match 31.5%; Score 450.5; DB 8; Length 297;

Best Local Similarity 41.2%; Pred. No. 1.3e-30;
 Matches 120; Conservative 38; Mismatches 82; Indels 51; Gaps 13;

5 VPQLQPNSQGGQPPQGVPLVQGGQPPGQGGQPPQGPYGPQGPFSQGPYQLGP-FQ 63
 18 IAGVETIPGLRPMQGGQPPQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 71
 64 PXLGPYGPQGPFPQGPYGPQGPYGPQGPYGPQGPYGPQGPYGPQGPYGPQGP 116
 72 ---QPLFSQGGQPPVLPQGPSSQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 125
 117 QI-----LQQQLIPGMDVVLQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 170
 126 QLNPCKVFLQGG---CSPVMPGH---LARSQGMQSSGCMVQGGQGGQGGQGG 179
 171 AIENVAIILHQQK-----QQQPSQGV-SFGQPLQ--QVPLGGGSGF-----RP 213
 180 AIRAIRPSIILQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 239
 214 SQGNPQAGSVQPPQGLPQFEIRNLALQTLPMCNVYIAPYCTI--APPGI 262
 240 QGGQVQXGTFLOQHQAIRLEVMISIALRTLPYCMCNVYIAPYSSITAPLGV 290

RESULT 7
 ID ADH89338 standard; protein; 307 AA.

XX ADH89338;

XX 06-MAY-2004 (first entry)

XX T. aestivum LMW glutenin-1D1 protein.

XX double stranded RNA; storage protein; 2S-albumen; 7S-globulin;
 XX 11S/12S-globulin; zein-prolamine; homogenisate; metabolic pathway;
 XX pharmaceutical; plant; abiotic stress; fatty acid composition; colour;
 XX lipid composition; oil composition; carbohydrate composition; colour;
 XX pigmentation; pathogen resistance; fruit ripening delay; aging;
 XX male sterility; lignin; fibre; cotton; Vitamin E synthesis; nicotine;
 XX caffeine; theophylline; threonine biosynthesis; glutennin.

XX Triticum aestivum.

XX WO2003078629-A1.

XX 25-SEP-2003.
 PD 17-MAR-2003; 2003WO-EP002735.
 XX PF 20-MAR-2002; 2002DB-01012892.
 XX PR (BADI) BASF PLANT SCT GMBH.
 PA Kock M, Bauer J;
 XX MPI; 2003-803869/75.
 DR N-PSDB; ADH89337.
 XX
 PT Reducing expression of at least two target genes, useful e.g. for
 PT producing transgenic plants, using partly double-stranded interfering
 PT RNA.
 PS Disclosure; SEQ ID NO 113; 228bp; German.
 XX
 CC This invention describes a novel method for reducing the expression of at
 CC least two different endogenous target genes in a eukaryotic cell or
 CC organism by introducing an RNA molecule that is at least partly double
 CC stranded. The transcribed RNAs from at least two target genes have
 CC homology below 90% and the RNA molecule is formed as a single, self-
 CC complementary molecule. At least one of the double-stranded structures
 CC formed from individual sense sequences has an even number of repeats of
 CC 21 or 22 bp. The RNA molecule may include an intron-encoding sequence. At
 CC least two target genes are selected from different classes of storage
 CC protein genes, i.e. 2S-albumen, 7S- or 11S/12S-globulins or zein-
 CC prolamine and at least one of the sense sequences is identical to storage
 CC protein sequences or genes in the homogenistate metabolic pathway or
 CC enzyme types, e.g. acetyl transacylases, thioesterases, (de)branching
 CC enzymes or cellulases. The RNA of the invention, also related cassettes,
 CC preparation systems, vectors and transgenic organisms are used for
 CC preparation of pharmaceuticals, in biotechnological processes and plant
 CC biotechnology, specifically in plants to improve protection against
 CC abiotic stress, to modify composition and/or content of fatty acids,
 CC lipids and oils, to modify carbohydrate composition, to alter colour or
 CC pigmentation, to reduce content of storage proteins, to increase
 CC resistance to pathogens, to inhibit stem break, to delay fruit ripening
 CC or aging, to induce male sterility, to reduce content of toxic or
 CC unwanted components, to modify lignification and/or lignin content, to
 CC modify the fibre component in foods or fibre quality in cotton, to reduce
 CC susceptibility to shock, to increase synthesis of Vitamin E, to reduce
 CC contents of nicotine, caffeine or theophylline and to increase methionine
 CC content, by reducing theanine biosynthesis. The method provides a rapid
 CC and efficient way of reducing gene expression, can inhibit more than one
 CC target gene, prevents development of multiple phenotypes (since the
 CC transcription rate is the same for all RNA sequences), significantly
 CC reducing the selection process required to produce an organism with
 CC effective suppression of all target genes), avoids problems of epigenetic
 CC gene silencing, does not require synthesis of individual RNA sequences
 CC and the method can be applied to plants with complex (polyploid) genomes.
 CC No interference between the individual RNA sequences occurs. This sequence
 CC represents a protein encoded by a target gene used in the method of the
 CC invention.
 XX
 XX Sequence 307 AA;
 Query Match 30.8%; Score 440.5; DB 7; Length 307;
 Best Local Similarity 42.8%; Pred. No. 1e-29;
 Matches 125; Conservative 37; Mismatches 75; Indels 55; Gaps 16;
 QY 13 PSQQQPOBQVPLVQCGQFP-----GQQQGFPPQPPQPPFSSQGYLQGFPPQPKLP 67
 Db 27 PQLERPMQGGPLPPQGTFFPQQPLRSQQGQ---QLLFQGGPSFSSQGGQ-----FFWQQGPP 78
 QY 68 YPQPSFPQPGP-----YPQPPQYSGPPQPI-----SQQAQQGQQGQQGQQGQQGQ 114
 Db 79 FSGQQPPIFPQGFSSQGGQLVLPQ-QPFFSQGGQPPVLPQPSPPQGGQGHQGLVQQQILP 137
 QY 115 -LQGLLQGLLFCMDVVLQGH--NIAG-----ASQVLAQSTVQLGLCCGHLMLQIPRQS 167

Db 138 VQPSIILQQLNFC-KVFLQGGCCFVAMPRLASSQMLQSSCHVMQGCCQQLPQIPQOS 196
 QY 168 QCGAIIHNVVAIILHQGQKQGGQSSQVSPQGFQGVPLGQGSFSPSQGNPQ-----219
 Db 197 RYEAIRAIIVSILL--QEQGQVQSISQGGQPPQ---LQCCVSPQGGSCQQLGGQPPQ 251
 QY 220 --AQGS-VQPGQLPQFESIRNALQTLPMKCNVYIAPV--CTIAPPGIFGT 265
 Db 252 QQLAQGTFLQPHQIAQLEVMVTSIALRILPTMCSVNVPLVYRTTTSVDFGV-GT 302
 RESULT 8
 ADG44134
 ID ADG44134 standard; protein; 307 AA.
 AC ADG44134;
 DT 26-FEB-2004 (first entry)
 XX
 DE T. aestivum glutenin-1D1 protein.
 XX
 KW oil content; plant; storage protein; seed-specific promoter; 2S-albumin;
 KW 7S-globulin; 11S-globulin; 12S-globulin; zein-prolamine; transgenic;
 KW oil production; fat production; free fatty acid production; food;
 KW animal feed; pharmaceutical; fine chemical production; glutenin.
 OS Triticum aestivum.
 XX
 PN WO2003077643-A2.
 XX
 PD 25-SEP-2003.
 XX
 PF 17-MAR-2003; 2003WO-EP002733.
 XX
 PR 20-MAR-2002; 2002DB-01012893.
 XX
 XX (BADI) BASF PLANT SCT GMBH.
 PA Bauer J;
 XX MPI; 2004-011485/01.
 DR N-PSDB; ADG44133.
 XX
 PT Increasing total oil content of plants, useful e.g. as foods or animal
 PT feeds, by reducing amount of storage proteins, particularly with double-
 PT stranded interfering RNA.
 XX
 XX Claim 4; SEQ ID NO 174; 253bp; German.
 CC This invention describes a novel method for increasing the total oil
 CC content of a plant by reducing the amount of at least one storage protein
 CC in the plant (or its tissue, organs, parts or cells) and selecting plants
 CC that have higher total oil content than starting plants. The storage
 CC protein is suppressed by introducing antisense RNA, optionally combined
 CC with a ribozyme, sense RNA that induces co-suppression, DNA-binding
 CC factors directed against storage protein genes, viral sequences that
 CC degrade storage protein RNA, constructs that induce homologous
 CC recombination of endogenous storage protein genes or mutations into
 CC storage protein genes. Most preferably a plant cell is stably transfected
 CC with a recombinant expression construct, then regenerated to plants that
 CC express the incorporated sequence. The expression constructs particularly
 CC contain a seed-specific promoter and they are introduced into plants by
 CC standard methods, e.g. via Agrobacterium. The preferred storage proteins
 CC of the invention are 2S-albumens, 7S or 11S/12S-globulins or zein-
 CC prolamines. Transgenic organisms produced by the new method are used for
 CC production of oils, fats, free fatty acids or their derivatives, useful
 CC as foods, animal feeds, pharmaceuticals and fine chemicals. This sequence
 CC represents a storage protein used to illustrate the method of the
 CC invention.
 XX
 XX Sequence 307 AA;

Query Match 30.8%; Score 440.5; DB 8; Length 307;
 Best Local Similarity 42.8%; Pred. No. 1e-29;
 Matches 125; Conservative 37; Mismatches 75; Indels 55; Gaps 16;

CC 13 PSQQQPEQEVPLVQGGQFF-----GQQQGFPPQGPYPQPPPSQGPYLQQLPFPQKLP 67
 CC 27 PGLERPMQGPPLPQGPFPQGPPLFSQQQ-----QQFPQGPSPSQGP-----PFWQQGP 78
 CC 68 YPQGPFPQGP-----YPQGPQYSGPQGP-----SQQAQGGGQGGGQGGGQGGGQ 114
 CC 79 PSQQQPLPQGPSPSQGGQLVLPQ-QPSPSQGGQPLPQGPSPFPQGGQGGQLVQGGQIP 137
 CC 115 -LQQLIPQGGQLPQMDVVLQGH--NIAF-----ARQVLAQSTYQLQELCCGHLAQIPRQS 167
 CC 138 VWPSPILQGLNFC-KVFLQGGQSPVAMPQRLARSGWLQSSCHVWQGGCCGQLPQIPQGS 196
 CC 168 QCAHNVVHAIIHMQGKQGGQSSQVSPFPQPLQGYPLGQGSFSPSQNP-----219
 CC 197 REAIAIYISIL--QEQGVQGSISQGGQPPQ---LQGVSPQGPQGGQGGQLGQGPQ 251
 CC 220 ---AGGS-VQPPQLPQFEIRMLAQTLPRMGNVYIAPY--CTIAPFGIGT 265
 CC 252 QQLAGSTPLQPHQIAQLFVMTSIALRIPLTMCSSVNPPLVRTTTSVPFGV-GT 302

RESULT 9
 AD071661 standard; protein; 298 AA.
 AD071661;
 12-AUG-2004 (first entry)
 Amino acid sequence of glutenin clone LMW6.
 low molecular weight subunit; LMW subunit; glutenin;
 wheat cultivar Cheyenne; gliadin; flour; tablet; coeliac disease;
 gluten intolerance.
 Triticum sp.
 Key Location/Qualifiers
 Disulfide-bond 25
 Disulfide-bond /note = this residue forms an intermolecular disulfide
 bond
 Disulfide-bond 227
 Disulfide-bond /note = this residue forms an intermolecular disulfide
 bond

EP1424342-A1.
 02-JUN-2004.
 27-NOV-2002; 2002EP-00026461.
 27-NOV-2002; 2002EP-00026461.
 (BAKE-) BAKEMARK DEUT GMBH.
 (MONS) MONSANTO AGRAR DEUT GMBH.
 (UNIF-) UNIFERN GMBH & CO KG.
 (PURA-) PURATOS NV.
 Hinzmann E, Wieser H, Stahl U;
 WPI: 2004-402870/38.
 N-PSDB; AD071660.
 Novel nucleic acid comprising sequence encoding modified glutenin
 polypeptide, useful for preparing modified glutenin polypeptide as
 gliadin substitute in foodstuffs such as dough, pastries and wafers.
 Example 1; Fig 5; 43pp; English.

CC The present sequence represents a low molecular weight (LMW) subunit of
 CC glutenin and is derived from clone LMW6 which is isolated from wheat
 CC cultivar Cheyenne. The LMW6 polypeptide does not contain the allergenic
 CC epitope QQQPP, and shows some minor differences to published sequences.
 CC It therefore represents a new allele for LMW subunit genes. The LMW6
 CC polypeptide was modified to produce modified glutenin polypeptides of the
 CC invention. In these modified polypeptides one or more cysteine residues
 CC responsible for intermolecular cross linking through disulfide bridges
 CC are deleted or substituted. The modified glutenin polypeptide is useful
 CC as a gliadin substitute. It is also useful in the preparation of
 CC foodstuffs, such as flour or for the preparation of pharmaceutical
 CC products, such as tablets, where the foodstuffs contain a considerably
 CC reduced amount of gliadin proteins or no gliadin proteins. Pharmaceutical
 CC compositions comprising the modified polypeptide of the invention are
 CC useful for treating patients suffering from coeliac disease or persons
 CC who are intolerant to gluten.

Sequence 298 AA;
 Query Match 30.6%; Score 437.5; DB 8; Length 298;
 Best Local Similarity 41.0%; Pred. No. 1.8e-29;
 Matches 118; Conservative 35; Mismatches 74; Indels 61; Gaps 13;

CC 13 PSQQQPEQEVPLVQGGQFFGQQQGFPPQGPYPQPPPSQGPYLQQLPFPQKLP 71
 CC 27 PGLERPMQGPPLPQGPFPQGPPLFSQQQ-----GQQGFPPQGPPLPQGPSPSQ-----QP 74
 CC 72 GSFPQGPYPQGPQYSGPQGPPLPQGPQGAQGGQGGQGGQGGQGGQGGQGGQGGQGGQ 118
 CC 75 LFSQKQGPYLQGPAPASQGGQGYLPPQGPAPASQGGQHQLQGLIPIVHPSILQGLNPKVF 134
 CC 119 LQGLIPQMDVVLQGHNIAHNSQVLAQSTYQLQELCCGHLAQIPRQSQCAHNVVHA 178
 CC 135 LQQQ---GSFVAMPQH---LARSQMWQSSCHVWQGGCCGQLPQIPRQSRVFAIPIFS 188
 CC 179 ITHHQGK-----GQQGPPSSQVS-----FQGP-QQYVLAGGSPSPSQ 216
 CC 189 ITHQGGQGVQPPQGGQPPQGGQVGVQPPQGGQGGQGGQGGQGGQGGQGGQGGQGGQ 243
 CC 217 NPQAGSVQPPQLPQFEIRMLAQTLPRMGNVYIAPYCTI--APFGI 262
 CC 244 QVQKGTFLQPHQIAQLFVMTSIALRIPLTMCSSVNPPLVYSITSAPFGV 291

RESULT 10
 ABB71695 standard; protein; 1798 AA.
 ABB71695;
 26-MAR-2002 (first entry)
 Drosophila melanogaster polypeptide SEQ ID NO 41877.
 Drosophila melanogaster polypeptide; cell signalling; insecticide;
 pharmaceutical.
 Drosophila melanogaster.
 WO200171042-A2.
 27-SEP-2001.
 23-MAR-2001; 2001WO-US009231.
 23-MAR-2000; 2000US-0191637P.
 11-JUL-2000; 2000US-00614150.
 (PEKE) PE CORP NY.
 Venter JC, Adams M, Li PMD, Myers EM;
 WPI: 2001-656860/75.

DR N-PSDB; ABL15798.
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 41877; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 1798 AA;

Query Match 20.1%; Score 287.5; DB 4; Length 1798;
 Best Local Similarity 37.3%; Pred. No. 1.2e-15;
 Matches 100; Conservative 19; Mismatches 92; Indels 57; Gaps 12;
 QY 3 VPVPLQPPNP-SQQQPPQGVPLVQ-----QQQPPQGGQPPPPQ 41
 DB 264 VGGATGPPQGSFQKPIPTDPPVQAVLSRSLSSNODSLMRQQLKQQQQMQQQQ 323
 QY 42 PYPQPPPP-SQQPPLQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 96
 DB 324 MAPPQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGGQGG 361
 QY 97 QQAQQ 152
 DB 362 QQQ 440
 QY 153 QELCCGHLMOIPBEGSCCAHNVVHAHILHQQGQQQQQQSSQVFPQPLQYPLGGGSR 212
 DB 441 -----ALQKQQQ-----LLHVQGGQAGQQPQQQQGRTVQQLPFAQQQQQL 480
 QY 213 PQQQNPQAQGVQPPQLPQFEIRIAL 240
 DB 481 PQQHVVQQQ---QPPGV-QFTQQGQIAL 504

RESULT 11
 ABB63057
 ID ABB63057 standard; protein; 2285 AA.
 XX
 AC ABB63057;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15963.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 FN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-UTL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li FWD, Myers EW;

XX WPI; 2001-656660/75.
 DR N-PSDB; ABL07160.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 15963; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 2285 AA;

Query Match 18.9%; Score 271; DB 4; Length 2285;
 Best Local Similarity 35.7%; Pred. No. 4e-14;
 Matches 101; Conservative 14; Mismatches 104; Indels 64; Gaps 13;
 QY 7 QLOPPNP-----SQQQPPQGVPLVQGGQPPPPPPPPPPPPPPPPPP 54
 DB 909 QMQQQPPVAVATVAVHGVMPQQGVN--QQQQPPQMQQIPQGVVQPPVPLPPPPHQQP 966
 QY 55 YLQQLPPPP-----PKLPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 99
 DB 967 QQQQQPQQ 1024
 QY 100 QQQ 153
 DB 1025 QQAQQQQQQSPLQIQQLIQQLQGVAVSHQQQIMQQLAHQQLQQLQQLQQLQQLQ 1084
 QY 154 ELCCGHLMOIPBEGSCCAHNVVHAHILHQQGQQQQQQSSQV---SQQPLQ---QY 204
 DB 1085 QIQQQQLQQLQQLQQLQ-QFVQGVQA--MPQCHQQLVTGSQVAFPHQHQPPIDIPVQM 1141
 QY 205 PL-----GGGFRSQGNPPQAQGVQPPQLPQF 232
 DB 1142 PPTSVAPPIQHTVYQGGQVTLSDAQQQCHGFSAVPQAPF 1184

RESULT 12
 AAY96255
 ID AAY96255 standard; protein; 1162 AA.
 XX
 AC AAY96255;
 XX
 DT 12-SEP-2003 (revised)
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Kaposi's sarcoma-associated herpesvirus LANA.
 XX
 KW Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
 KW latency-associated nuclear antigen; LANA; gamma-2 herpes virus;
 KW Human herpes virus 8; HHV8; rhadino virus cis-acting element; KVCAB;
 KW Kaposi's sarcoma; primary effusion lymphoma; PEL;
 KW human immunodeficiency virus; HIV; multicentric Castleman's disease.
 XX
 OS Human herpesvirus 8.
 XX
 FH Key
 FT Domain
 FT Domain
 FT Domain
 FT Domain
 FT Region
 Location/Qualifiers
 14..17
 /note="nuclear localisation signal, NLS"
 64..70
 /note="nuclear localisation signal, NLS"
 320..429

CC (S2) as a cis-acting and maintenance sequence in the DNA. (A) is
 CC particularly used in gene therapy (or other gene transfer applications)
 CC that uses mammalian cells in which LANA is expressed. (A) improves
 CC persistence of gene therapy vectors in cells. The present sequence
 CC represents Kaposi's sarcoma-associated herpesvirus (KSHV, also called
 CC human herpesvirus 8) LANA protein, which is used in the exemplification
 CC of the present invention
 CC
 CC

XX
 SQ Sequence 1162 AA:

Query Match 18.9%; Score 270; DB 5; Length 1162;

Best Local Similarity 38.0%; Pred. No. 2,3e-14;

Matches 93; Conservative 20; Mismatches 100; Indels 32; Gaps 10;

```

4 PVPQLPQNPSQQQPPQEQVPLVQ--QQQPPSQQ--QFPFPQPPYPQPPFPSPQPPYLQ 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
495 PLQEPQQQEPQQQEPQQQEPQQQEPQQQEPQQQEPQQQEPQQQEPQQQEPQQQEPQQQ 553
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
60 P---PQQPKLKY---PQ---PQSFPQQPPYPQF-QPYQSPPQPPISQQQAQQQQQQQQQQ 109
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
554 PQQREPPQRRPPQRRPPQRRPPQRRPPQRRPPQRRPPQRRPPQRRPPQRRPPQRRPPQ 613
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
110 QQQQILQQQLIQQLIPQMDVYLQHNIAHRSQVLAQSTYQLQLCCGHLMLQIPQSGC 169
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
614 EQQDEQQQDEQQ---ODEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQ 663
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
170 QAIHNVYHAIILHQKKKQQQQPPSSQVSFOQPLQGYPLAQGSFRPSQNNPQAQGSVQPPQL 229
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
664 EQQD-----EQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQ 716
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
230 PQFES 234
   | : |
717 EQQD 721

```

Search completed: December 14, 2004, 17:17:27
 Job time : 77.6667 secs

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OW protein - protein search, using sw model

Run on: December 14, 2004, 17:06:20 ; Search time 19 Seconds
(without alignments)
928.452 Million cell updates/sec

Title: US-10-089-700-3-K65

Perfect score: 1431

Sequence: 1 VRVVPOLQPNPSQQQPOE.....CNVYIAPYCTIAPFGIFGTN 266

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cg2_6/ptodata/1/aa/5B.COMB.pep.*
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4: /cg2_6/ptodata/1/aa/6B.COMB.pep.*
5: /cg2_6/ptodata/1/aa/PTUS.COMB.pep.*
6: /cg2_6/ptodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	464	33.4	369	2	US-08-991-300-2
2	270	18.9	1162	2	US-08-728-333A-2
3	270	18.9	1162	3	US-09-298-568-2
4	270	18.9	1162	4	US-09-410-399-2
5	270	18.9	1162	4	US-09-899-273-2
6	249	17.4	788	2	US-08-918-914-4
7	234	16.4	256	4	US-09-248-796A-21251
8	232	16.2	498	4	US-09-270-767-45042
9	217.5	15.2	579	4	US-09-668-119-3
10	217	15.2	2074	4	US-09-491-356C-9
11	202	14.1	2023	4	US-09-491-356C-8
12	202	14.1	2124	4	US-09-538-092-1377
13	198.5	13.9	505	4	US-09-248-796A-19253
14	197.5	13.8	663	4	US-09-270-767-61220
15	197.5	13.8	1591	4	US-09-270-767-45698
16	197.5	13.8	2441	1	US-08-194-468-2
17	197.5	13.8	2441	1	US-08-961-739-2
18	197.5	13.8	2441	3	US-09-514-247A-8
19	197.5	13.8	2441	3	US-09-686-316-2
20	196.5	13.7	379	4	US-09-248-796A-23759
21	196.5	13.7	2442	3	US-09-514-247A-10
22	196.5	13.7	2442	3	US-09-538-092-1370
23	196.5	13.7	216	4	US-09-248-796A-21017
24	195.5	13.7	729	3	US-09-625-188-20
25	188	13.1	295	4	US-09-248-796A-20004
26	187.5	13.1	320	4	US-09-248-796A-24758

28	184.5	12.9	316	4	US-09-270-767-42663	Sequence 42663, A
29	184.5	12.9	332	4	US-09-248-796A-21649	Sequence 21649, A
30	184	12.9	519	4	US-09-248-796A-19263	Sequence 19263, A
31	178	12.4	382	4	US-09-248-796A-22236	Sequence 22236, A
32	178	12.4	408	4	US-09-248-796A-14480	Sequence 14480, A
33	178	12.4	1319	4	US-09-538-092-1291	Sequence 1291, A
34	177	12.4	261	4	US-09-602-565-34	Sequence 34, A
35	177	12.4	657	4	US-09-248-796A-19232	Sequence 19232, A
36	177	12.4	848	4	US-09-538-092-33	Sequence 33, A
37	176.5	12.3	684	4	US-09-248-796A-15319	Sequence 9, A
38	176	12.3	618	4	US-09-248-796A-18720	Sequence 18720, A
39	174.5	12.2	382	4	US-09-514-259-37	Sequence 37, A
40	173	12.1	1507	4	US-09-248-796A-27827	Sequence 27827, A
41	171.5	12.0	311	2	US-08-853-310-2	Sequence 2, A
42	171.5	12.0	903	2	US-09-248-796A-20699	Sequence 20699, A
43	171	11.9	675	4	US-08-718-661-2	Sequence 2, A
44	170.5	11.9	667	2	US-09-698-295-10	Sequence 10, A
45	168	11.7	2781	4		

ALIGNMENTS

RESULT 1
US-08-991-300-2
Sequence 2, Application US/08991300
Patent No. 5973225
GENERAL INFORMATION:
APPLICANT: D'OVIDIO, RENATO
APPLICANT: PORCEDDU, ENRICO
APPLICANT: MERCHETTI, CINZIA
APPLICANT: CARDELLI, LUISA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, WAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,300
FILING DATE: 16-DEC-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-0201-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-300-2
Query Match 32.4%; Score 464; DB 2; Length 369;
Best Local Similarity 40.2%; Pred. No. 6,7e-35;

US-09-410-399-2
; Sequence 2, Application US/09410399
; Patent No. 6482587
; GENERAL INFORMATION:
; APPLICANT: Robertson, Erle S.
; APPLICANT: Cotter, Murray A.
; TITLE OF INVENTION: Methods to Inhibit or Enhance the Binding of Viral DNA
; TITLE OF INVENTION: to Genomic Host DNA
; FILE REFERENCE: UM-03778
; CURRENT APPLICATION NUMBER: US/09/410,399
; CURRENT FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-410-399-2

Query Match 18.9%; Score 270; DB 4; Length 1162;
Best Local Similarity 38.0%; Pred. No. 1.9e-16;
Matches 93; Conservative 20; Mismatches 100; Indels 32; Gaps 10;

QY 4 FVPLQPPNPPSQQQPQOEPLVQ--QQQPPQQ--QQPPQQPPPPPPSQPPQLQ 59
DB 495 PLOEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQ 553
QY 60 P---PPOKLPY---PQ---PQSFPQQPPYPQP-QPQYSPQQPISQQQAQQQQQQQQQ 109
DB 554 PQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQ 613
QY 110 QQQQILQQILQQILPCMDVVLQGHNIARSGVLQOSTYQLLQELCCQHLWQIPESQC 169
DB 614 EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 663
QY 170 QAHNVVHAIIILHQKQKQKQSSQVSFQQPLQYLGGSFPPSQQNPQAQGSVPQQL 229
DB 664 EQQD-----EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQD 716
QY 230 PQEE 234
DB 717 EQQD 721

RESULT 5
US-09-894-273-2
; Sequence 2, Application US/09894273
; Patent No. 6756203
; GENERAL INFORMATION:
; APPLICANT: Kieff, Elliott D.
; APPLICANT: Bailettas, Mary E.
; APPLICANT: Kaye, Kenneth M.
; TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO
; TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE
; FILE REFERENCE: 16412-10001R
; CURRENT APPLICATION NUMBER: US/09/894,273
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 60/109,422
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO: 2
; LENGTH: 1162
; TYPE: PRT
; ORGANISM: Kaposi's sarcoma-associated herpesvirus
US-09-894-273-2

Query Match 18.9%; Score 270; DB 4; Length 1162;
Best Local Similarity 38.0%; Pred. No. 1.9e-16;
Matches 93; Conservative 20; Mismatches 100; Indels 32; Gaps 10;
4 FVPLQPPNPPSQQQPQOEPLVQ--QQQPPQQ--QQPPQQPPPPPPSQPPQLQ 59

DB 495 PLOEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQ 553
QY 60 P---PPOKLPY---PQ---PQSFPQQPPYPQP-QPQYSPQQPISQQQAQQQQQQQQQ 109
DB 554 PQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQEPQQ 613
QY 110 QQQQILQQILQQILPCMDVVLQGHNIARSGVLQOSTYQLLQELCCQHLWQIPESQC 169
DB 614 EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQ 663
QY 170 QAHNVVHAIIILHQKQKQKQSSQVSFQQPLQYLGGSFPPSQQNPQAQGSVPQQL 229
DB 664 EQQD-----EQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQDEQQD 716
QY 230 PQEE 234
DB 717 EQQD 721

RESULT 6
US-08-918-914-4
; Sequence 4, Application US/08918914
; Patent No. 5876963
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Peter
; APPLICANT: Hutchinson, Nancy
; APPLICANT: Lawton, Michael
; APPLICANT: Magna, Holly
; APPLICANT: Yocum, Sue
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: HUMAN NUCLEOTIDE PYROPHOSPHORYLASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,914
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 788 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 107094
US-08-918-914-4

Query Match 17.4%; Score 249; DB 2; Length 788;
Best Local Similarity 31.0%; Pred. No. 1e-14;
Matches 89; Conservative 23; Mismatches 97; Indels 78; Gaps 10;

Db 1847 000PAVPGORLNO--L00S0GMLG0SSVH0MTSSSVGL0TS0GYPPVSVHGL00HT 1904
 QY 44 -----PQPFPSQ0PFLQ0LPFPQPLPYF-----QPSFPPQ0PVP----- 81
 Db 1905 GRAGTWPPSYSSQ0PQSTHPTNPVTUPPTNHL0QRBSGYH0QAPYTHGHLSTQSPS 1964
 QY 82 ----QPQYSQ-----PQPISSQ0A000000000000000000000000000000 117
 Db 1965 H0TL0QTPMISTMTWPSAGVAGVSTALPE0000000000000000000000000000 2024
 QY 118 -LLOQGLPCMDVVLQ0HNIAHRSQVLOQSTYCL0ELCC0HMC0IE0SGCC0A1HNVV 176
 Db 2025 HIR000-----Q00ILR000000000000000000000000000000000000 2062
 QY 177 HAILH000K000-----QPS0VSFQ-QPQQYPLGSGSFRPSQ0NPOA0G5V0PQ 227
 Db 2063 -----H0000000A0P0CQ0P0S0P0F0SG0GL0Q0T00000TALVR0LQ00L0SNT0PQ 2115

RESULT 13

US-09-248-796A-19253
 Sequence 19253, Application US/09248796A
 Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 19253

LENGTH: 505

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-19253

Query Match

Best Local Similarity 13.9%; Score 198.5; DB 4; Length 505;
 Best Local Similarity 27.1%; Pred. No. 2,6e-10;
 Matches 64; Conservative 24; Mismatches 47; Indels 101; Gaps 7;

QY 4 PVP-----QHPQNPSSQ0QPE0VPLV000QFP00000PFP00PYP0PQPFPSQ0PYLQ0 59
 Db 365 PVPNMLB0L00000Q00 401
 QY 60 PFPQPKLPYQ0P0SFP0Q0P0P0P0P0P0P0P0P0P0P0P0P0P0P0P0P0P0P0P0 119
 Db 402 -----EPQ0P0Q0E0Q0E0Q0E0Q0E0Q0E0Q0E0Q0E0Q0E0Q0E0Q0E0Q0E0 451
 QY 120 C00GLPCMDVVLQ0HNIAHRSQVLOQSTYCL0ELCC0HLM0IE0SGCC0A1HNVVHAI 179
 Db 452 Q00-----PDPQ0EE----- 461
 QY 180 ILH000K000Q0P0S0VSF0Q0P0Q0YPLGSGSFRPSQ0NPOA0G5V0P00L0P0FEI 235
 Db 462 ---Q00EK0P0P00 503

RESULT 14

US-09-270-767-61220
 Sequence 61220, Application US/09270767
 Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 61220
 LENGTH: 663
 TYPE: PRT
 ORGANISM: Drosophila melanogaster
 US-09-270-767-61220

Query Match 13.8%; Score 197.5; DB 4; Length 663;
 Best Local Similarity 29.8%; Pred. No. 4,4e-09;
 Matches 88; Conservative 25; Mismatches 97; Indels 85; Gaps 13;

QY 4 PVPQLOP0NPSSQ0QPE0VPLV000QFP00000PFP00PYP0P0P0P0P0P0P0P0P0 63
 Db 195 PVAE---EE0 242
 QY 64 PKLPYQ0P0SFP0Q0P0 105
 Db 243 --LPAP0HRSVNPQ-----Q0000H0P0YVIEB0P0KLIBE0LQARAVH0L0R0000H0 296
 QY 106 Q000 154
 Db 297 Q000 350
 QY 155 LC-----C0HLM0IE0SGCC0A1HNVVHAIILH000K000Q0P0S0VS 196
 Db 351 LVTPTYSHPRG0PKYLP0A0QIQ0ED000000P0R0V0LHKPITP0P0Q0LHGLP0IA 410
 QY 197 P00P0Q0YPLGSGSFRPSQ0NPOA0G5V0P0Q0P0FEIRNAL0TUPAMCNVYI 251
 Db 411 Y0QP-----Q1SYKTLPNHPLAKSSLE-----SEIEKLIANKRQ0SLAVY 451

RESULT 15

US-09-270-767-45698
 Sequence 45698, Application US/09270767
 Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 45698

LENGTH: 1591

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-45698

Query Match

Best Local Similarity 13.8%; Score 197.5; DB 4; Length 1591;
 Best Local Similarity 29.8%; Pred. No. 1,3e-09;
 Matches 88; Conservative 25; Mismatches 97; Indels 85; Gaps 13;

QY 4 PVPQLOP0NPSSQ0QPE0VPLV000QFP00000PFP00PYP0P0P0P0P0P0P0P0P0 63
 Db 1123 PVAE---EE0 1170
 QY 64 PKLPYQ0P0SFP0Q0P0 105
 Db 1171 --LPAP0HRSVNPQ-----Q0000H0P0YVIEB0P0KLIBE0LQARAVH0L0R0000H0 1224
 QY 106 Q000 154
 Db 1225 Q000 1278
 QY 155 LC-----C0HLM0IE0SGCC0A1HNVVHAIILH000K000Q0P0S0VS 196
 Db 1279 LVTPTYSHPRG0PKYLP0A0QIQ0ED000000P0R0V0LHKPITP0P0Q0LHGLP0IA 1338
 QY 197 P00P0Q0YPLGSGSFRPSQ0NPOA0G5V0P0Q0P0FEIRNAL0TUPAMCNVYI 251
 Db 1339 Y0QP-----Q1SYKTLPNHPLAKSSLE-----SEIEKLIANKRQ0SLAVY 1379

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Page 7

Search completed: December 14, 2004, 17:29:03
Job time : 20 secs

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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1345.5	94.0	287	17	US-10-739-930-5777	Sequence 9777, Apr
2	1244.5	86.7	339	17	US-10-739-930-5619	Sequence 9619, Apr
3	1244	86.7	288	17	US-10-739-930-5770	Sequence 9770, Apr
4	590	41.12	337	17	US-10-739-930-5623	Sequence 9623, Apr
5	558.5	39.0	282	17	US-10-474-955-101	Sequence 101, Apr
6	547.5	38.3	288	17	US-10-739-930-5621	Sequence 9621, Apr
7	526	36.8	279	17	US-10-474-955-99	Sequence 99, Apr
8	525	36.7	279	17	US-10-474-955-97	Sequence 97, Apr
9	521	36.4	279	17	US-10-474-955-98	Sequence 98, Apr
10	521	36.4	279	17	US-10-474-955-100	Sequence 100, Apr
11	448.5	31.3	304	17	US-10-739-930-5782	Sequence 9782, Apr
12	440.5	30.8	307	17	US-10-739-930-5782	Sequence 9782, Apr
13	384	26.8	244	17	US-10-739-930-5769	Sequence 9769, Apr

14	274	19.4	53.1	17	US-10-423-115-200100	Sequence 200100
15	277	19.1	123.1	17	US-10-422-115-600097	Sequence 200097
16	270	18.9	112.1	11	US-09-894-803-2	Sequence 2
17	270	18.9	112.2	14	US-10-294-804-2	Sequence 2, Appl.
18	266.5	18.6	106.9	14	US-10-161-997-54	Sequence 54, Appl.
19	257	18.0	223.5	15	US-10-422-114-44003	Sequence 44003, Appl.
20	251	17.5	90.5	16	US-10-451-467A-64	Sequence 64, Appl.
21	248.5	17.4	390	15	US-10-424-599-370450	Sequence 270450, Appl.
22	241	16.8	358	14	US-10-104-047-3710	Sequence 3710, Appl.
23	239.5	16.7	229	15	US-10-425-114-11056	Sequence 41056, Appl.
24	231.5	16.2	148	14	US-10-465-217-15	Sequence 15, Appl.
25	231	16.0	104.4	15	US-10-425-114-72709	Sequence 72709, Appl.
26	229.5	15.0	362	17	US-10-423-115-261231	Sequence 261231, Appl.
27	227	15.9	73.8	16	US-10-451-467A-238	Sequence 238, Appl.
28	226.5	15.8	113.3	16	US-10-431-963-1434743	Sequence 144743, Appl.
29	225.5	15.8	192	15	US-10-425-114-52411	Sequence 52411, Appl.
30	224	15.7	123.6	10	US-09-763-787-109	Sequence 109, Appl.
31	222	15.5	102.4	16	US-10-479-546-12	Sequence 12, Appl.
32	222	15.5	113.3	16	US-10-479-546-1	Sequence 1, Appl.
33	221.5	15.5	164.5	15	US-10-263-929-176	Sequence 176, Appl.
34	219	15.3	495.2	15	US-10-051-874-56	Sequence 56, Appl.
35	219	15.3	500.8	15	US-10-051-874-165	Sequence 165, Appl.
36	219	15.3	519.9	15	US-10-085-188-112	Sequence 112, Appl.
37	219	15.3	526.2	15	US-10-051-874-165	Sequence 165, Appl.
38	219	15.3	526.2	15	US-10-051-874-165	Sequence 165, Appl.
39	218	15.2	351	15	US-10-264-049-2693	Sequence 2693, Appl.
40	216.5	15.1	1351.7	15	US-10-283-122A-75147	Sequence 75147, Appl.
41	214	15.0	1343.5	15	US-10-283-122A-75965	Sequence 75965, Appl.
42	214	15.0	1362	9	US-09-815-243-14009	Sequence 14009, A
43	213.5	14.9	1365	16	US-10-437-963-190032	Sequence 190032, Appl.
44	212.5	14.8	99.4	15	US-10-421-114-55600	Sequence 55600, Appl.
45	209.5	14.6	105.5	16	US-10-437-963-1153116	Sequence 1153116, Appl.

ALIGNMENTS

RESULT 1
US-10-739-930-9777
; Sequence 9777, Application US/10739930

1. TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT

CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

LENGTH: 287

ORGANISM: *Triticum aestivum*

OTHER INFORMATION: Clone ID: TRIAE-23APR03-C176_238.f
; RS-10-739-930-9777

Query Match	94.0%;	Score 1345.5;	DB 17;	Length 287;
Best Local Similarity	95.1%;	Pred. No. 3.6e-98;		
Matches 254;	Conservative 1;	Mismatches 12;	Indels 1;	Gaps 1

1 VRVPVQLQPQNPSQQQFQEQVPLVQQQFPGQQQFPPQQQPYQPQPFPSPQQPYLQLQF 60

21 VRFPVQLPQNPSQQLPQEQVPLVQQQQLGQQQPFPPQQQPYPPQPFPSPQLPYLQLP 80

61 FRQPKLPYRQSFPRQRPQRYSPQRPSQQAQQQQQQQQQLQQLQ 120

81 FPGPGLPYSQPPFRPQPPYPQPPQYSQPPPISSQQQQQQQQQQQQQQQQILQLQ 140

121 QQLPCMDVVLQOHNIAHARSQVLQOSTYOLLQELCCQHLWQIPEQSQCQAIHNVHAI I 180

141 QQLPCMDVVLQQHNIAHGRSQVLQQSTYQLLQELCCQHLWQIPEQSQCAIHNVVHAI I 200


```

; Sequence 101, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Driffoht, Jan W.
; APPLICANT: Konig, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 101
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of GAMMA-1
US-10-474-955-101

```

```

Query Match          39.0%; Score 558.5; DB 17; Length 282;
Best Local Similarity 47.6%; Pred. No. 4e-36;
Matches 138; Conservative 33; Mismatches 72; Indels 47; Gaps 15;

```

```

QY 2 RVVPVQL---QPQNSQQPQEQGVPLVQQQPFQ---PPQPYPPQ-QPFS 51
DB 10 QVPMVQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 68
QY 52 --QQPVYQ--LQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 106
DB 69 QPQVYPPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 118
QY 107 QQQQVQLQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQ 162
DB 119 FQQQVQLQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQ 178
QY 163 IPEQSCCAHNVVAIILHQQKQQQSSQVFSQQL-QQVPLGGGSRPQONPQA 221
DB 179 IPQQLQCAHNVVAIILHQQKQQQSSQVFSQQL-QQVPLGGGSRPQONPQA 229
QY 222 GSVQVQLQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 264
DB 230 GIVQVQLQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 279

```

```

RESULT 6
US-10-739-930-9621
; Sequence 9621, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 9621
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Triticum aestivum
; FEATURE:
; OTHER INFORMATION: Clone ID: TRIA-23APR03-C125_65.p
US-10-739-930-9621

```

```

Query Match          38.3%; Score 547.5; DB 17; Length 298;
Best Local Similarity 46.9%; Pred. No. 3.1e-35;
Matches 134; Conservative 29; Mismatches 74; Indels 49; Gaps 14;
4 PVPQLQPNPQQPQEQGVPLVQQQPFQ---PPQPYPPQPFQPFQPFQ 61

```

```

DB 36 PVP---QPHQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 84
QY 62 P-QPQLPYPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 110
DB 85 PQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 140
QY 111 QQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQ 166
DB 141 QPPIQSLQQVPCNFKFLQCKPVSLSVSMISVMSVDCQVWRQCCQQLAQIPQ 200
QY 167 SQCCAHNVVAIILHQQKQQQSSQVFSQQL-QQVPLGGGSRPQONPQA 225
DB 201 LQCAHNVVAIILHQQKQQQSSQVFSQQL-QQVPLGGGSRPQONPQA 251
QY 226 PQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 264
DB 252 PQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 279

```

```

RESULT 7
US-10-474-955-99
; Sequence 99, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:
; APPLICANT: Driffoht, Jan W.
; APPLICANT: Konig, Frits
; APPLICANT: McAdam, Stephan N.
; APPLICANT: Ludwig, Solid Magne
; TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
; FILE REFERENCE: 2799/71244-PCT-US
; CURRENT APPLICATION NUMBER: US/10/474,955
; CURRENT FILING DATE: 2003-10-13
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 99
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of GAMMA-4
US-10-474-955-99

```

```

Query Match          36.8%; Score 526; DB 17; Length 279;
Best Local Similarity 46.2%; Pred. No. 1.4e-33;
Matches 132; Conservative 27; Mismatches 75; Indels 52; Gaps 14;

```

```

QY 4 PVPQLQPNPQQPQEQGVPLVQQQPFQ---PPQPYPPQPFQPFQPFQ 61
DB 18 PVP---QPHQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 66
QY 62 P-QPQLPYPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 110
DB 67 PQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 122
QY 111 QQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQ 166
DB 123 QPPIQSLQQVPCNFKFLQCKPVSLSVSMISVMSVDCQVWRQCCQQLAQIPQ 182
QY 167 SQCCAHNVVAIILHQQKQQQSSQVFSQQL-QQVPLGGGSRPQONPQA 225
DB 201 LQCAHNVVAIILHQQKQQQSSQVFSQQL-QQVPLGGGSRPQONPQA 230
QY 226 PQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 264
DB 231 PQQPQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQPFQ 276

```

```

RESULT 8
US-10-474-955-97
; Sequence 97, Application US/10474955
; Publication No. US20040241161A1
; GENERAL INFORMATION:

```

APPLICANT: Drifftout, Jan W.
 APPLICANT: Konig, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solliid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 97
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Consensus amino acid sequence
 US-10-474-955-97

Query Match 36.7%; Score 525; DB 17; Length 279;
 Best Local Similarity 46.2%; Pred. No. 1.7e-33;
 Matches 132; Conservative 27; Mismatches 75; Indels 52; Gaps 14;

DB 4 PVPQLQPQNPSSQOQPEQVPLVQOQOFPQOQOQFP--PQQPYQPQPFPSQOQPYLQLPF 61
 18 PVP--QPHQPFQOQ-----QTFPQOQTFHQPQOQPFQOQ--PQOQFLQOQPF 66
 QY 62 P-QPKLPYQOQSPFPQOQPYQOQ-----PQYSPQOQPIQOQOQ-----QOQOQOQOQ 110
 DB 67 PQOQOQPYQOQ-----QOQOQPFQOQOQFLPQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 122
 QY 111 QOQILQOQILQOQILPQMDVYLQOQHN-----IAHARSQVLTQOQSTYQLQOELCCOHLQOIPQ 166
 DB 123 QPFFIQLQOQVNPCKNPLQOQCKPVSIVSLSMIMIPQSDQVWRQOQCOQLAQIPQ 182
 QY 167 SQCCAIHNVVHAIIHQQOQKQOQOQSSQVSFQOQPL-QOYPLQOQSRPSQOQNPQOQSGVQ 225
 DB 183 LQCCAIHNVHSHIIMQOQOQOQ-----GWHILPLVQOQOQVQOQTL-----VOGQGITQ 230
 QY 226 PQQLPQOFEIRNLALQTLPMQCNVYIAPYCTI--APF-----GIFG 264
 DB 231 PQQPAQLQALRSLVLTQTLPTMCNVYVPPQCSIIKAPFSSVAVGIG 276

RESULT 9
 US-10-474-955-98
 Sequence 98, Application US/10474955
 Publication No. US20040241161A1
 GENERAL INFORMATION:
 APPLICANT: Drifftout, Jan W.
 APPLICANT: Konig, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solliid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 98
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of GAMMA-2
 US-10-474-955-98

Query Match 36.4%; Score 521; DB 17; Length 279;
 Best Local Similarity 45.8%; Pred. No. 3.6e-33;
 Matches 131; Conservative 27; Mismatches 76; Indels 52; Gaps 14;

4 PVPQLQPQNPSSQOQPEQVPLVQOQOFPQOQOQFP--PQQPYQPQPFPSQOQPYLQLPF 61

DB 18 PVP--QPHQPFQOQ-----QTFPQOQTFHQPQOQPFQOQ--PQOQFLQOQPF 66
 QY 62 P-QPKLPYQOQSPFPQOQPYQOQ-----PQYSPQOQPIQOQOQ-----QOQOQOQOQ 110
 DB 67 PQOQOQPYQOQ-----QOQOQPFQOQOQFLPQOQOQOQOQOQOQOQOQOQOQOQOQOQOQ 122
 QY 111 QOQILQOQILQOQILPQMDVYLQOQHN-----IAHARSQVLTQOQSTYQLQOELCCOHLQOIPQ 166
 DB 123 QPFFIQLQOQVNPCKNPLQOQCKPVSIVSLSMIMIPQSDQVWRQOQCOQLAQIPQ 182
 QY 167 SQCCAIHNVVHAIIHQQOQKQOQOQSSQVSFQOQPL-QOYPLQOQSRPSQOQNPQOQSGVQ 225
 DB 183 LQCCAIHNVHSHIIMQOQOQOQ-----GWHILPLVQOQOQVQOQTL-----VOGQGITQ 230
 QY 226 PQQLPQOFEIRNLALQTLPMQCNVYIAPYCTI--APF-----GIFG 264
 DB 231 PQQPAQLQALRSLVLTQTLPTMCNVYVPPQCSIIKAPFSSVAVGIG 276

RESULT 10
 US-10-474-955-100
 Sequence 100, Application US/10474955
 Publication No. US20040241161A1
 GENERAL INFORMATION:
 APPLICANT: Drifftout, Jan W.
 APPLICANT: Konig, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solliid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 100
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of GAMMA-3
 US-10-474-955-100

Query Match 36.4%; Score 521; DB 17; Length 279;
 Best Local Similarity 46.0%; Pred. No. 3.6e-33;
 Matches 131; Conservative 29; Mismatches 75; Indels 50; Gaps 14;

DB 4 PVPQLQPQNPSSQOQPEQVPLVQOQOFPQOQOQFP--PQQPYQPQPFPSQOQPYLQLPF 61
 DB 18 PVP--QPHQPFQOQ-----QTFPQOQTFHQPQOQPFQOQ--PQOQFLQOQPF 66
 QY 62 P-QPKLPYQOQ-----PQYSPQOQPYQOQ-----PQYSPQOQPIQOQOQ-----QOQOQOQOQ 110
 DB 67 PQOQOQPYQOQOQFLPQOQ 123
 QY 112 QOQILQOQILQOQILPQMDVYLQOQHN-----IAHARSQVLTQOQSTYQLQOELCCOHLQOIPQ 167
 DB 124 PPFILQOQVNPCKNPLQOQCKPVSIVSLSMIMIPQSDQVWRQOQCOQLAQIPQ 183
 QY 168 SQCCAIHNVVHAIIHQQOQKQOQOQSSQVSFQOQPL-QOYPLQOQSRPSQOQNPQOQSGVQ 226
 DB 184 LQCCAIHNVHSHIIMQOQOQOQ-----GWHILPLVQOQOQVQOQTL-----VOGQGITQ 231
 QY 227 PQQLPQOFEIRNLALQTLPMQCNVYIAPYCTI--APF-----GIFG 264
 DB 232 PQQPAQLQALRSLVLTQTLPTMCNVYVPPQCSIIKAPFSSVAVGIG 276

No.	Score	Match Length	DB	ID	Description
1	1364	95.3	286	2	S07923
2	1356	94.8	288	1	ESWTA
3	1312	91.7	288	2	T066282
4	1267.5	88.6	291	2	T06498
5	1267.5	88.6	307	2	S10015
6	1263	88.3	296	2	S07361
7	1261	88.1	313	2	S07924
8	1257	87.8	296	2	A27319
9	1248.5	87.2	319	2	A22364
10	1245.5	87.0	319	2	C22364
11	1235.5	86.3	297	2	T06500
12	1233	86.5	326	2	D22364
13	1206	84.3	320	2	E22364
14	1183	82.7	282	2	T06504
15	1155.5	80.7	292	2	B22364
16	589	41.2	327	2	JS04402
17	549.5	38.4	291	1	ESWGT
18	541	37.8	302	2	TA0152
19	486	34.0	305	2	S08312
20	469	32.8	286	2	T05718
21	461.5	32.3	374	2	T05923
22	457.5	32.0	359	2	T06982
23	454.5	31.8	356	2	S01992
24	448.5	31.3	304	2	T06505
25	447	31.2	293	2	S07365
26	445	31.1	264	2	S07975
27	443	31.0	286	2	T05910
28	442	30.9	288	2	S20853
29	441.5	30.9	298	2	T06980

EMBO J. 3, 1409-1415, 1984

Query Match 88.6%; Score 1267.5; DB 2; Length 307;

Best Local Similarity .84.7%; Pred. No. 2.7e-77;
Matches 243; Conservative 9; Mismatches 14; Indels 21; Gaps 3

```

QY 1 VAVPVADQIQKNPSQSQQFOEQVPLVQSQQFQSQSQQFPPQDPFYQDPFPSSQDPYQLQDP 60
Db 21 VAVPVADQIQKNPSQSQQFOEQVPLVQSQQFQSQSQQFPPQDPFYQDPFPSSQDPYQLQDP 80
QY 61 F-----PQKLPYQDPQSFPPQDPYQDPQYQSQQFQSQSQQSQQSQQSQQSQQSQQSQQSQQSQQ 105
Db 81 FQDPQLFPYQDPFYQDPFYQDPFYQDPFYQDPFYQDPFYQDPFYQDPFYQDPFYQDPFYQDPFYQDP 140
QY 106 ---QQQQQQQQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQIIQQII 163
Db 141 QKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 200
QY 164 PEOSSQCAIHNVVAIIILH-----QQQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 219
Db 201 PEOSSQCAIHNVVAIIILHQQQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQKQK 260
QY 220 AGGSVVPQQLPQFEERINLAQTTPAMCMVYAPACTIAPGIGIN 266
Db 261 AGGSVVPQQLPQFEERINLAQTTPAMCMVYAPACTIAPGIGIN 307

```

RESULT 6
S07361
alpha/beta-gliadin precursor (clone pM1215) - wheat

C/Species: *Triticum aestivum* (common wheat)
C/Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C/Accession: S07361
R/Submitter-Smith, M., Rafalski, J.A.; Sugiyama, T.; Stoll, M.; Soell, D.
Nucleic Acids Res. 13, 3305-3316, 1985
A/Title: Conservation and variability of wheat alpha/beta-gliadin genes.
A/Reference number: S07361; MUID:85242077; PMID:3839304
A/Accession: S07361
A/Status: preliminary
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-296 <SUM>
A/Cross-references: UNIPROT:P04726; EMBL:X02538; NID:g21756; PIDN:CAA26383.1; PID:g21757
C/Superfamily: gliadin
C/Keywords: seed; storage protein

	Query Match Similarity	88.3%	Score 1263:	DB 2:	Length 296:	
	Best Local Similarity	88.1%	Pred. No. 5.2e-77:			
	Matches 244:	Conservative	5;	Mismatches 16;	Indels 12;	Gaps 4
QY	1	VRVVPQLQPONPSQQCPQEIVPLVQQQQPFGCQQCPFPPOQFPPPOPFPDPFPSPCCPYLLQLQP	60			
Ds	21	VRVPQPPQPNPSQPFQCGVPLVQQQQCFPGCQQCFPPQCPFPPOPFPSPCCPYLLQLQP	80			
QY	61	FPPQ-----PKLPPQSPFPFPPOPFPPOPFPSPQCFPSQQQA----QQGQQCQQCQQQQ	111			
Ds	81	FPPQPPFPFPQFLYPQDPPFPSPQCFIPQDPPQFPQDPPFSQQQAQQGQQCQQCQQCQQQQ	140			
QY	112	QCILLQQILLQQILLPCMDVVLLQGHINIAHARSQVLQGSTYGLLELCQHIMQIPEGSQCA	171			
Ds	141	COILLQQILLQQILLPCRDVLLQGHINIAHARSQVLQGSTYLPDLQCCQIQMLQIPEGRCA	200			
QY	172	IHNVAHALILHQGXKQQQQSSQVSFQCPLOQVPLFCQSFRPSSQNPFCAQSGSVQEPQLDQ	231			
Ds	201	IHNVAHALILHQQR-QQQPSSQVSLQQRQQQYPSQGGFFGQGNQNPQAGSVQEPQLDQ	259			
QY	232	FEIRNLALQTLPMACNVTIAPYC--TTPFGIGCTN	266			
Ds	260	FEIRNLALQTLPRMCNVYIIPKCSTLIAPFGIGCTN	296			

RESULT 7
S07924
alpha/beta-gliadin precursor - wheat
CISpecies: Triticum aestivum (common wheat)
CDate: 08-Jun-1994 #sequence_revision 01-Dec-1995 #next_change 09-Jul-2004
CJAccession: S07924; C61218

Risumner-Smith, M.; Rafalski, J.A.; Sugiyama, T.; Stoll, M.; Soell, D.
Nucleic Acids Res. 13, 3905-3916, 1985

[illegible]

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RESULT 8
A27319
gliadin - wheat
CISpecies: Triticum aestivum (common wheat)
C>Date: 04-Mar-1988 #sequence_revision 04-Mar-1988 #text_change 03-Feb-1994
C:Accession: A27319
R:Reeves, C.D.; Okita, T.M.
Gene 52, 257-266, 1987
A:Title: Analyses of alpha/beta-type gliadin genes from diploid and hexaploid wheats
A:Reference number: A27319; MUID:87277398; PMID:3038685
A:Accession: A27319
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-296 <RFE>
C:Superfamily: gliadin

```

	Query Match	87.8%;	Score 1257;	DB 2;	Length 256;										
	Best local Similarity	87.7%;	Pred. No. 1.3e-76;												
	Matches 223;	Conservative	4;	Mismatches 18;	Indels 12;										
				Gaps	4										
Qy	1	VAVPVQLP	QKMPKQQQ	QEQEVLVQQQ	QFPGQQQ	QFPPOQ	QYPCQ	QFPFSCQ	CPYQLQ	LP	60				
Db	21	VAVPVQ	QPPQKPSQ	QKQFQV	QVPLVQQQ	QFPGQQQ	QFPFQ	QYPCQ	QFPFSCQ	PYQLQ	80				
Qy	61	FPQ----	EKLPPQ	QDSFP	QQPYQ	QFQDS	QPCQ	PISSQ	QCA---	QQQQQ	QQQQQQ	111			
Db	81	FPQ	QEPFQ	PLP	PPQ	CPFP	SPQ	QYPCQ	QFQV	QPCQ	PISSQ	QCAQQQQ	QQQQQQ	QQQQQQ	140

QY 112 QGILLQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 171
DB 141 QGILLQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 200
QY 172 HNVVHAIIILHQQQVQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 231
DB 201 HNVVHAIIILHQQQVQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 259
QY 232 FEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 266
DB 260 FEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 296

RESULT 9
alpha/beta-gliadin precursor (clone A42) - wheat
Nucleotide names: prolamins
C/Spectrum: Triticum aestivum (common wheat)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A22364
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: A22364
A/Molecule type: mRNA
A/Residues: 1-319 <OKI>
A/Cross-references: UNIPROT:P04725; GB:M11073; NID:g170715; PID:AAA4278.1; PID:g170716
C/Superfamily: gliadin
E/21-319/Product: alpha/beta-gliadin #status predicted <SIG>
E/21-319/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 87.2%; Score 1248.5; DB 2; Length 319;
Best Local Similarity 81.9%; Pred. No. 5,1e-76;
Matches 245; Conservative 6; Mismatches 15; Indels 33; Gaps 4;

QY 1 VAVPVQLQPNPSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 60
DB 21 VAVPVQLQPNPSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 80
QY 61 FPGQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQ 114
DB 81 FPGQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQ 140
QY 115 LQQLIQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 174
DB 141 LQQLIQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 200
QY 175 VHAIIILH-----QQQKQQQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 209
DB 201 VHAIIILH-----QQQKQQQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 260
QY 210 SFRPSQGNPQAQGSVQPLQQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 266
DB 261 SFRPSQGNPQAQGSVQPLQQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 319

RESULT 10
alpha/beta-gliadin precursor (clone A212) - wheat
Nucleotide names: prolamins
C/Spectrum: Triticum aestivum (common wheat)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A22364
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: A22364
A/Molecule type: mRNA
A/Residues: 1-319 <OKI>
A/Cross-references: UNIPROT:P04722
C/Superfamily: gliadin
E/1-20/Domain: signal sequence #status predicted <SIG>

F/21-319/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 87.0%; Score 1245.5; DB 2; Length 319;
Best Local Similarity 80.3%; Pred. No. 8e-76;
Matches 242; Conservative 8; Mismatches 16; Indels 33; Gaps 4;

QY 1 VAVPVQLQPNPSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 60
DB 21 VAVPVQLQPNPSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 80
QY 61 FPGQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQ 114
DB 81 FPGQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQ 140
QY 115 LQQLIQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 174
DB 141 LQQLIQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 200
QY 175 VHAIIILH-----QQQKQQQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 209
DB 201 VHAIIILH-----QQQKQQQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 260
QY 210 SFRPSQGNPQAQGSVQPLQQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 266
DB 261 SFRPSQGNPQAQGSVQPLQQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 319

RESULT 11
alpha/beta-gliadin A-IV precursor - wheat
Nucleotide names: prolamins
C/Spectrum: Triticum aestivum (common wheat)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06500
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: T06500
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-297 <OKI>
A/Cross-references: UNIPROT:P04724; EMBL:M11075; NID:g170723; PID:AAA4282.1; PID:g170724
C/Superfamily: gliadin
C/Keywords: seed; storage protein
E/1-297/Product: signal sequence #status predicted <SIG>
E/21-297/Product: alpha/beta-gliadin A-IV #status predicted <MAT>

Query Match 86.3%; Score 1235.5; DB 2; Length 297;
Best Local Similarity 84.3%; Pred. No. 3.4e-75;
Matches 236; Conservative 10; Mismatches 17; Indels 17; Gaps 3;

QY 1 VAVPVQLQPNPSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 60
DB 21 VAVPVQLQPNPSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 80
QY 61 F-----PQPLPYQPSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 113
DB 81 FPGQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQPLPQ 137
QY 114 LQQLIQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 173
DB 138 LQQLIQQLIPGMDVVLQGHNIHAARSQVLTQSTYQLLQELCCGHLMOQIPESQCOA 197
QY 174 HNVVHAIIILH-----QQQKQQQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 226
DB 198 HNVVHAIIILH-----QQQKQQQSSQVSPQQLQQLYLGSGSFRPSQGNPQAQGSVQPLQ 257
QY 227 QQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 266
DB 258 QQLPQFEIRNLALQTLPAKCNVYIAPYC--TIAPFGIFGTN 297

RESULT 12

D22364
alpha/beta-gliadin precursor (clone A735) - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: D22364
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: D22364
A/Molecule type: mRNA
A/Residues: 1-326 <OKI>
A/Cross-references: UNIPROT:P04724
C/Superfamily: gliadin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-326/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 85.5%; Score 1223; DB 2; Length 326;
Best Local Similarity 77.8%; Pred. No. 2.5e-74;
Matches 238; Conservative 10; Mismatches 18; Indels 40; Gaps 4;

QY 1 VRVVPVQLQPONSQQQPPQEVPLVQQQQPPGQQQQPPPPQQPPQPPPPSQQPPYQLQGP 60
DB 21 VRVVPVQLQPONSQQQPPQEVPLVQQQQPPGQQQQPPPPQQPPQPPPPSQQPPYQLQGP 80
QY 61 F-----PPPLPYQPQSPFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 107
DB 81 FPPQPQPPPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 140
QY 108 QQQQQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQL 167
DB 141 QQQQQQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQL 200
QY 168 QQQQIHNVVAIIILH-----QQQKQQQPPSSQVSPQPPQ 202
DB 201 RCQAHNVVAIIILHQQ 260
QY 203 QYPLPGSP 260
DB 261 QYPLPGSP 320
QY 261 GIGFTN 266
DB 321 GIGFTN 326

RESULT 13

E22364
alpha/beta-gliadin precursor (clone A1235) - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: E22364
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: E22364
A/Molecule type: mRNA
A/Residues: 1-320 <OKI>
A/Cross-references: UNIPROT:P04723
C/Superfamily: gliadin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-320/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 84.3%; Score 1206; DB 2; Length 320;
Best Local Similarity 79.0%; Pred. No. 3.3e-73;
Matches 237; Conservative 12; Mismatches 17; Indels 34; Gaps 5;

QY 1 VRVVPVQLQPONSQQQPPQEVPLVQQQQPPGQQQQPPPPQQPPQPPPPSQQPPYQLQGP 59
DB 21 VRVVPVQLQPONSQQQPPQEVPLVQQQQPPGQQQQPPPPQQPPQPPPPSQQPPYQLQGP 80
QY 60 PFPQ-----PKLVPQPSFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 113

DB 81 PFPQPPPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 140
QY 114 ILQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQL 173
DB 141 TLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQL 200
QY 174 NVVAIIILH-----QQQKQQQPPSSQVSPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 208
DB 201 NVVAIIILHQQ 260
QY 209 GSFPSP 266
DB 261 VSPQSP 320

RESULT 14

T06504
alpha/beta-gliadin precursor (A-III) - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C/Accession: T06504
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: T06504
A/Status: preliminary; translated from GB/EMBL/DDJ
A/Molecule type: mRNA
A/Residues: 1-282 <OKI>
A/Cross-references: UNIPROT:P04723; EMBL:M11076; NID:g170725; PIDN:AAA34283.1; PID:g17
C/Superfamily: gliadin
C/Keywords: seed; storage protein
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-282/Product: alpha/beta-gliadin A-III #status predicted <MAT>

Query Match 82.7%; Score 1183; DB 2; Length 282;
Best Local Similarity 84.8%; Pred. No. 9.9e-72;
Matches 228; Conservative 12; Mismatches 19; Indels 10; Gaps 4;

QY 1 VRVVPVQLQPONSQQQPPQEVPLVQQQQPPGQQQQPPPPQQPPQPPPPSQQPPYQLQGP 59
DB 21 VRVVPVQLQPONSQQQPPQEVPLVQQQQPPGQQQQPPPPQQPPQPPPPSQQPPYQLQGP 80
QY 60 PFPQKLYPPQPPSP 119
DB 81 PFP-PQLPYPQPPPPQPPPPQPPPPQPPPPQPPPPQPPPPQPPPPQPPPPQPPPPQPPPPQPP 133
QY 120 QQLLIPCMNVVLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLL 179
DB 134 QQLLIPCMNVVLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLL 193
QY 180 ILHQQQKQQQQSSQVSPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 239
DB 194 ILHHHQQQQQSSQVSPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 253
QY 240 LQTLPMCMNVVLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLL 266
DB 254 LQTLPMCMNVVLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLLQQLL 282

RESULT 15

B22364
alpha/beta-gliadin precursor (clone A26) - wheat
C/Species: Triticum aestivum (common wheat)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: B22364
R/Okita, T.W.; Cheesbrough, V.; Reeves, C.D.
J. Biol. Chem. 260, 8203-8213, 1985
A/Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA
A/Reference number: A92541; MUID:85234522; PMID:2989281
A/Accession: B22364
A/Molecule type: mRNA

A:Residues: 1-292 <OKI>
A:Cross-references: UNIPROT:P04721

C:Superfamily: gliadin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-292/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match

80.7%; Score 115.5; DB 2; Length 292;

Best Local Similarity 84.1%; Pred. No. 6.8e-70; Mismatches 9; Indels 31; Gaps 4;

Matches 227; Conservative 3;

```

  1 VRVVPVQLCPNPSCQEQEQLVYQQQQFRGQQQCFPPQCPYPQCPFPSPQPYLQLQP 60
  21 VRVVPVQLCPNPSCQEQEQLVYQQQQFRGQQQCFPPQCPYPQCPFPSPQPYLQLQP 80
  61 F--PQ---PCLPYPCQSFPPQCPYPQCPYPQCPYIS-QQQACQQQQQQQQQQQQQ 114
  81 FLQPPPPPPPLPYSQPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 140
  115 LQQILQQQLPCMDVVLQGHNTAHARSQLQGSTYQLQELCCQHLWQIFEOSCCAIHN 174
  141 IQQILQQQLPCMDVVLQGHNTAHARSQLQGSTYQLQELCCQHLWQIFEOSCCAIHN 200
  175 VVHAIIILH-----QQQKQQQPPSSQVSTFQPLQGYPLGCG 209
  201 VVHAIIILHQQQQQQQQQQEQKQLQQQQQQQQQLQQQQQQQQQQPPSSQVSTFQPLQGYPLGCG 260
  210 SFRPSQNPQAQGSVQPPQLPQFEETRNLA 239
  261 SFRPSQNPQAQGSVQPPQLPQFEETRNLA 290
```

Search completed: December 14, 2004, 17:27:01
Job time : 16 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 17:01:05 ; Search time 79 Seconds
(without alignments)
1937.337 Million cell updates/sec

Title: US-10-089-700-3-K65
Perfect score: 1431
Sequence: 1 VRRVPPQLQPONPSQQQPOE.....CNYTAPYCTIAPFGIFGTN 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02:.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1368	95.6	269	2	Q9M4L7
2	1356	94.8	286	1	GD40_WHEAT
3	1356	94.8	286	2	AAA96525
4	1354	94.6	288	2	Q9ZP09
5	1350.5	94.4	274	2	Q9M4M5
6	1350.5	94.4	276	2	Q9M4M2
7	1345.5	94.0	287	2	Q41509
8	1344	93.9	277	2	Q9M4L8
9	1341.5	93.7	276	2	Q9M4M0
10	1337.5	93.5	289	2	Q41531
11	1330.5	93.0	270	2	Q9M4L9
12	1328.5	92.9	278	2	Q9M4M1
13	1328.5	91.9	259	2	Q41533
14	1312	91.7	288	2	Q41530
15	1299.5	90.8	287	2	Q41528
16	1267.5	88.6	290	2	Q9M4L6
17	1267.5	88.6	291	1	GD42_WHEAT
18	1267.5	88.6	307	1	GD49_WHEAT
19	1263	88.3	296	1	GD46_WHEAT
20	1262	88.2	313	1	GD47_WHEAT
21	1261	88.1	313	2	Q41546
22	1257	87.8	296	2	Q41632
23	1254	87.6	273	2	Q9M4M4
24	1249	87.3	318	2	Q41545
25	1248.5	87.2	319	1	GD45_WHEAT
26	1246	87.1	313	2	Q41529
27	1235.5	86.3	297	1	GD44_WHEAT
28	1200.5	83.9	262	1	GD41_WHEAT
29	1197	83.6	265	2	Q9M4M3
30	1193	83.4	265	2	Q9M4M6
31	1183	82.7	282	1	GD43_WHEAT

32	933	65.2	186	1	GD48_WHEAT	P04728	triticum	ae
33	594.5	41.5	455	2	Q9FR41	Q9FR41	secale	cere
34	590	41.2	308	2	Q9M6P7	Q9M6P7	triticum	ae
35	590	41.2	311	2	Q9M6P9	Q9M6P9	triticum	ae
36	590	41.2	327	1	Q94G91	Q94G91	triticum	ae
37	589	41.2	327	1	GD42_WHEAT	GD42	triticum	ae
38	581	40.6	337	2	Q94G96	Q94G96	triticum	ae
39	569	39.8	300	2	Q9FEA8	Q9FEA8	aequilops	bi
40	569	39.8	300	2	Q9FUA1	Q9FUA1	aequilops	lo
41	558.5	39.0	274	2	Q6EEW0	Q6EEW0	triticum	ae
42	558.5	39.0	282	2	Q6EEW7	Q6EEW7	triticum	ae
43	558.5	39.0	298	2	Q94G92	Q94G92	triticum	ae
44	556.5	38.9	275	2	Q6EEW4	Q6EEW4	triticum	tu
45	555	38.8	275	2	Q6EEW2	Q6EEW2	triticum	tu

ALIGNMENTS

RESULT 1

Q9M4L7 PRELIMINARY; PRT; 269 AA.

AC Q9M4L7 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Alpha-glutadin.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Mjcelner; TISSUE=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Sollied L.M.; (Mar-1999) to the EMBL/GenBank/DBJ databases.
 RL Submitted (Mar-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ13611; CAB/6963.1; -.
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001354; Gliadin.
 DR Pfam; PF00234; TYP_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SM00499; AAI; 1.
 FT CHAIN 1 269
 SQ SEQUENCE 269 AA; 31292 MW; 87127D6FD15EC78B CRC64;

Query Match 95.6%; Score 1368; DB 2; Length 269;
 Best Local Similarity 96.2%; Pred. No. 14e-75;
 Matches 256; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY	1	VRRVPPQLQPONPSQQQPOEYVLTQQQFPQQQQQFPQQQYPPQPPFPQQPYLQLQP	60
DB	2	VRRVPPQLQPONPSQQQPEQVPLVQQQFLQQQPFPPQQYPPQPPFPQQPYLQLQP	61
QY	61	PPQKPLPPQPSFPQQYPPQPPQYSPQPPPIQQQAQQQQQQQQQQQQQQQQQQQQQQ	120
DB	62	PPQPLPPQPSFPQQYPPQPPQYSPQPPPIQQQAQQQQQQQQQQQQQQQQQQQQQQ	121
QY	121	QQLIPGMDVVLQOHNIHARSQVLOOSTYQLQELCCOHLAQIPQSQCCALHNVAHAI	180
DB	122	QQLIPGMDVVLQOHNIHARSQVLOOSTYQLQELCCOHLAQIPQSQCCALHNVAHAI	181
QY	181	LHQOQKQKQKQSSQVFFQQLQYPIGGSFPSSQNPQASQVQPPQQLPQEEIRNLAL	240
DB	182	LHQOQKQKQKQSSQVFFQQLQYPIGGSFPSSQNPQASQVQPPQQLPQEEIRNLAL	241
QY	241	QTLPPACNVYIAPYCTIAPFGIFGTN	266
DB	242	QTLPPACNVYIAPYCTIAPFGIFGTN	267

RESULT 4					
ID	Q9ZP09	PRELIMINARY;	FRT,	288 AA.	
AC	Q9ZP09;				
DT	01-MAY-1999	(TREMBLrel. 10, Created)			
DT	01-MAY-1999	(TREMBLrel. 10, Last sequence update)			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)			
DE	Alpha-gliadin precursor (Fragment).				
CN	Name=alpha-gliadin;				
OS	Triticum aestivum subsp. spelta.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Triticeae; Triticum.				
OX	NCBI_TaxID=58933;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Kaserd D.D., D'Ovidio R.;				
RT	"Deduced amino acid sequence of an alpha-gliadin gene from Spelt wheat				
RT	(Spelta) includes sequences active in celiac disease."				
RL	Cereal Chem. 76:548-551(1999).				
DR	EMBL; AJ130948; CAA10257.1; -				
DR	PIR; S13333; S13333.				
DR	GO; GO:0045735; P:nutrient reservoir activity; IEA.				
DR	InterPro; IPR003612; AAI.				
DR	InterPro; IPR001376; Gliadin.				
DR	InterPro; IPR001954; Glia_gluutenin.				
DR	Pfam; PF00234; TRYP_alpha_amy1. 1.				
DR	PRINTS; PR00208; GLIADGLUTEN.				
DR	SMART; SM00493; AAI. 1.				
KM	Signal.				
FT	SIGNAL	1	20	Potential	
FT	CHAIN	21	>288	alpha-gliadin.	
FT	NON TER	288	288		
SQ	SEQUENCE	288 AA;	33203 MW;	DA058F3FAFA6BC6C CRC64;	
Query Match		94.6%;	Score 1354;	DB 2;	Length 288;
Best Local Similarity		95.1%;	Pred. No. 1e-74;		
Matches	255;	Conservative	1;	Mismatches	10;
				Indels	2;
				Gaps	1
QY	1 VAVPVQLQPQNPPSCQQPOEQVPLVQQQPFPGQQQFPDPQPYQPDPFPSSQPYTLQLP				60
DB	21 VAVPVQLQLOPNPSSQQQPOEQVPLVQQQFLGQQCFPPQCPYPQPPPSQOPYLQLQP				80
QY	61 FPOPKLPPYQPOSFPQQPYPPQYQOPYSQPPQPTIS--QQDAQQQQQQQQQQQQQOITLQOI				118
DB	81 FPQPOLPYSPQPPFRQCPYPPOPFPQYSPQPCPSQQQQQQQQQQQQQQQQQQQTLLQOI				140
QY	119 LQQQLPFCMDVVLQGNINIAHARSQVLAQSSTYQLIGELCCQHLWQIPESQCAIHNVVA				178
DB	141 LQQQLPFCMDVVLQGNINIAHGSRQVLAQSTYQLIGELCCQHLMQIREQSCQAIRHVVA				200
QY	179 ILHQQKXQQQPSQVSFOQPIQYYPLGGSTRPSEQNFPAGCSYQPPQLPFEETRNL				238
DB	201 ILHQQKXQQQPSQVSFOQPIQYYPLGGSTRPSEQNFPAGSVQPPQLPFEETRNL				260
QY	239 ALQTLPAQCNVYLAPYCTIAPEGIPTNN				266
DB	261 ALQTLPAQCNVYLPPYCTIIPFGIFGIN				288
RESULT 5					
ID	Q9M4M5	PRELIMINARY;	PRT;	274 AA.	
AC	Q9M4M5;				
DT	01-OCT-2000	(TREMBlrel. 15, Created)			
DT	01-OCT-2000	(TREMBlrel. 15, Last sequence update)			
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)			
DE	Alpha-gliadin.				
OS	Triticum aestivum (Wheat).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC	Triticeae; Triticum.				

Query	Match	Best Local Similarity	Score	Pred. No.	DB 2	Length	Gaps
Matches	255	Conservative	1	Mismatches	10	Indels	5
Query	1	VRVPPQLQPNPNSQCCQEQEVPLVQCCQCFQCCQCCQFPFQCPYPQPOBPFPSCQPYLQLP	60				
Db	2	VRVVPQQLQPNPNSQCCQEQEVPLVQCCQCFQCCQCCQFPFQCPYPQPOBPFPSCQPYLQLP	61				
Query	61	FPQPLPYPQPSFPFQCPYPQPOBPFPSCQPYLQLP	115				
Db	62	FPQPLPYPQPSFPFQCPYPQPOBPFPSCQPYLQLP	121				
Query	116	QQLLQQLLPCMDVYLQCHNIAHARSQVLAQSTYQLLQELCCQHLMOIPEQSCCAINNV	175				
Db	122	QQLLQQLLPCMDVYLQCHNIAHARSQVLAQSTYQLLQELCCQHLMOIPEQSCCAINNV	181				
Query	176	VHAILHQKQKQKQSSQVFSQPLQCPYLCQGSFRPSQNPQAQGSQVQPLQPFEL	235				
Db	182	VHAILHQKQKQKQSSQVFSQPLQCPYLCQGSFRPSQNPQAQGSQVQPLQPFEL	241				
Query	236	RNLALQTLPAWCVYIAPYCTAPGIGTIN	266				
Db	242	RNLALQTLPAWCVYIAPYCTAPGIGTIN	272				

[illegible]

OC Trifolium aestivum (Mead).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Trifolium.
OX NCBI_taxid=4565;
RN
RP SEQUENCE FROM N.A.
RA STRAIN=Micelner; TISSUE=Endosperm;
RA Arendt-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
RA Sollid L.M.;
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ133608; CAB76960.1; -
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001376; Gliadin.
DR InterPro; IPR001954; Glia glutenin.
DR Pfam; PF00234; Tryp_alpha_amy1; 1.
DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAI; 1.
FT CHAIN 1 276 alpha-gliadin.
SQ SEQUENCE 276 AA; 3221 MW; 6A2E9723D42B100A CRC64;

Query Match 93.7%; Score 1341.5; DB 2; Length 276;
Best Local Similarity 92.7%; Fred.No.57e-74;
Matches 253; Conservative 3; Mismatches 10; Indels 7; Gaps 1

DQ 1 VRVVPVLQPCQNSSQQCPQBOYVLVQOCCFPQCQCQCFPPQCPYPQPDPFFSQPVTQLQP 60
DQ 2 VRRPVPLQPCQNSSQQCPQBOYVLVQOCCFLGCGQPFPPQCPYPQPDPFFSQPVTQLQG 61
DY 61 PPOKLPYPPOGSFPPQCPYPQPDPQPSQCPPISQQAQQQQQQQQQQ-----QQ 113
DB 62 PPQQLSYSPQPFPPQCPYPQPDPQPSQCPPISQQAQQQQQQQQQQQQQQQQQQQQQQ 121
DY 114 ILQQLILQOQHILPCMDVYLQOHNTAHARSQVLQGSTYYLLQELCOHLMQIPESGCQAIH 173
DB 122 ILQQLILQOQHILPCMDVYLQOHNTAHARSQVLQGSTYYLLQELCOHLMQIPESGCQAIH 181
DY 174 NVVAATILHQOKXQOQOQSSQVSFPQPLQOYPLGGSFRRSQNPQAQGSVQPOLPQFE 233
DB 182 NVVAATILHQOKXQOQOQSSQVSFPQPLQOYPLGGSFRRSQNPQAQGSVQPOLPQFE 241
DY 234 FIRNLALQTLPMACNVYTIAPYCTIARFGIGFN 266
DB 242 FIRNLALQTLPMACNVYTIPEYCAMAFGIIFGN 274

RESULT 10
Q41531 PRELIMINARY; PRT; 289 AA.

ID Q41531;
AC Q41531;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DDT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DPT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Alpha-glialdin storage protein.
OS Trifolium aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Trifolium.
OX NCBI_TaxID=4565;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=Cheyenne;
RA Anderson O.D.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DDJ databases.
DR EMBL; U51306; AAA96524.1; -
DR PIR; S13333; S13333.
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR003612; AAI.
DR InterPro; IPR001376; Gliadin.
DR InterPro; IPR001954; Glia glutenin.
DR Pfam; PF00234; Tryp_alpha_amy1; 1

```

DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SW00499; AAI; 1.
SQ SEQUENCE 289 AA; 33349 MW; 5F577C9D63874FA CRC64;

Query Match 93.5%; Score 1337.5; DB 2; Length 289;
Best Local Similarity 94.1%; Pred. No. 1e-73;
Matches 253; Conservative 2; Mismatches 11; Indels 3; Gaps 1;

QY 1 VRVVPVPLQONPSSQQQPOECVPLVYQQQCFPGGQQCFPPPOQPYQPQPFPSQPFYLOLP 60
DB 21 VRVSVPLQONPSSQQQPOEQVPLVYQQQCFLGQQQPFPPQPPQPYQLQPFPSQPFYLOLP 80
QY 61 FPGPKLPYPOQSFPPQPPQPYQPQYSSQPPQPSIS---QQQAQQQQQQQQQQQQQQQQQ 117
DB 81 FPGQLPYPSQPQPFPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 140
QY 118 ILQQQLPCMDVYLQCHNIAHARSQVLAQSGTYQLQELCCGHLQIEPSQSCQA1HNHYH 177
DB 141 ILQQQLPCMDVYLQCHNIVHGRSQVLAQSGTYQLRLCCGHLQIEPQSCQA1HNHYH 200
QY 178 AIIHQOQKQQQSSQVSPFOQPLQOYPLQGGSFPSQONPQAQGSVQPPQLPQFEIRN 237
DB 201 AIIHQOQKQQQSSQVSPFOQPLQOYPLQGGSFPSQONPQAQGSVQPPQLPQFEIRN 260
QY 238 LALQTLPMACNVYIAFYCTIAPFQIFGYN 266
DB 261 LALQTLPMACNVYIPIYCTIAPFQIFGYN 289

RESULT 11
QSM4L9 PRELIMINARY; PRT; 270 AA.
ID QSM4L9
AC QSM4L9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Alpha-glutadin.
OS Triticum aestivum (wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4585;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mjcelner; TISSUE=Endosperm;
RA Arentz-Hansen E.H., McAdam S.N., Wolberg O., Kristiansen C.,
RA Soild L.M.;
RL Submitted (Mar-1999) to the EMBL/genbank/DBJ databases.
DR EMBL; AJ133609; CAB76961.1; -
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
DR InterPro; IPR001376; AAI.
DR InterPro; IPR001376; Gliadin.
DR InterPro; IPR001954; Glia_gluutenin.
DR Pfam; PF00234; TYP_alpha_amy1; 1.
DR PRINTS; PR00208; GLIADGLUTEN.
DR PRINTS; PR00209; GLIADIN.
DR SMART; SM00499; AAI; 1.
FT CHAIN 1 270 alpha-gliadin.
SQ SEQUENCE 270 AA; 31491 MW; 1DB4B6528EFA0PFS CRC64;

Query Match 93.0%; Score 1330.5; DB 2; Length 270;
Best Local Similarity 94.0%; Pred. No. 2.6e-73;
Matches 251; Conservative 4; Mismatches 11; Indels 1; Gaps 1;

QY 1 VRVVPQLOPQNPSSQQQPOEQVPLVYQQQCFPGQQQQCFPPQPPQPYQPQPFPSQPFYLOLP 60
DB 2 VRVSVPLQONPSSQQQPOEQVPLVYQQQCFLGQQQPFPPQPPQPPQPPQPPQPPQPPQPPQ 61
QY 61 FPGPKLPYPOQSFPPQPPQPYQPQYSSQPPQPSIS---QQQAQQQQQQQQQQQQQQQQQ 119
DB 62 FPGQLPYPSQPQPFPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 121

```

QY 120 QOOLIPCMQVYLQOHNIHARSQVYLGSTYQLQELCCQHLMOIPESQCCAIHNVHAI 179
 DB 122 QOOLIPCMQVYLQOHNIHARSQVYLGSTYQLQELCCQHLMOIPESQCCAIHNVHAI 181
 QY 180 IHQOQKQOQSSQVSPQPLQOYPLGSGSPRSCQNPQAGSVQPLQOYPLQOY 239
 DB 182 IHQOQKQOQSSQVSPQPLQOYPLGSGSPRSCQNPQAGSVQPLQOYPLQOY 241
 QY 240 IOTLPAMCNVYIAPYCTIAPFGIFGTN 266
 DB 242 IOTLPAMCNVYIAPYCTIAPFGIFGTN 268

RESULT 12

QY4M1 PRELIMINARY; PRT; 278 AA.

AC Q9M4M1; PRELIMINARY; PRT; 278 AA.
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DB Alpha-glialdin.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OC NCBI_Taxid=4565;

RA [1] SEQUENCE FROM N.A.
 RC STRAIN=Mjoleire; TISSUE=Endosperm;
 RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,
 RA Solild L.M.;
 DT Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
 DB EMBL; AJ133607; CAB76959.1; -;
 DB GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DB InterPro; IPR003612; AAI.
 DB InterPro; IPR001376; Gliadin.
 DB InterPro; IPR001954; Gliadin.
 DB Pfam; PF00234; Tryp_alpha_amy1; 1.
 DB PRINTS; PR00208; GLIADGLUTEN.
 DB PRINTS; PR00209; GLIADIN.
 DB SMART; SMO0499; AAI; 1.
 FT CHAIN 1 278 alpha-glialdin.
 SQ SEQUENCE 278 AA; 32502 MW; 30B5BFD10DC8A7D CRC64;

Query Match 92.9%; Score 1329.5; DB 2; Length 278;
 Best Local Similarity 92.0%; Pred. No. 3e-73;
 Matches 253; Conservative 2; Mismatches 11; Indels 9; Gaps 1;

QY 1 VAVPVQLQPNPSSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 60
 DB 2 VAVPVQLQPNPSSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 61
 QY 61 FPQPLPYQPSQPSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 111
 DB 62 FPQPLPYQPSQPSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 121
 QY 112 QOOLIPCMQVYLQOHNIHARSQVYLGSTYQLQELCCQHLMOIPESQCCAIHNVHAI 179
 DB 122 QOOLIPCMQVYLQOHNIHARSQVYLGSTYQLQELCCQHLMOIPESQCCAIHNVHAI 181
 QY 172 IHNVHAIHQQOQKQOQSSQVSPQPLQOYPLGSGSPRSCQNPQAGSVQPLQOYPLQOY 231
 DB 182 IHNVHAIHQQOQKQOQSSQVSPQPLQOYPLGSGSPRSCQNPQAGSVQPLQOYPLQOY 241
 QY 233 FEEIRNLALQTLFAMCNVYIAPYCTIAPFGIFGTN 266
 DB 242 FEEIRNLALQTLFAMCNVYIAPYCTIAPFGIFGTN 276

RESULT 13
 QY4M1 PRELIMINARY; PRT; 259 AA.
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DB Alpha-glialdin.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OC NCBI_Taxid=4565;

DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Alpha-glialdin (Fragment).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OC NCBI_Taxid=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98409296; PubMed=9738916;
 RA Maryama N., Ichise K., Katsube T., Kishimoto T., Kawase S.,
 RA Matsumura Y., Takeuchi Y., Sawada T., Utsumi S.;
 RT "Identification of major wheat allergens by means of the Escherichia
 RT coli expression system.";
 RL Eur. J. Biochem. 255:739-745 (1998).
 DR EMBL; D84341; BAA12318.1; -;
 DR GO; GO:0045735; F:nutrient reservoir activity; IEA.
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001376; Gliadin.
 DR InterPro; IPR001954; Gliadin.
 DR Pfam; PF00234; Tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00209; GLIADIN.
 DR SMART; SMO0499; AAI; 1.
 FT NON TER 1 259
 FT CHAIN 1 259 alpha-glialdin mature peptide.
 SQ SEQUENCE 259 AA; 29996 MW; F536CD48F8F54C6 CRC64;

Query Match 91.9%; Score 1315.5; DB 2; Length 259;
 Best Local Similarity 93.2%; Pred. No. 2e-72;
 Matches 248; Conservative 2; Mismatches 9; Indels 7; Gaps 1;

QY 1 VAVPVQLQPNPSSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 60
 DB 1 VAVPVQLQPNPSSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 60
 QY 61 FPQPLPYQPSQPSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 120
 DB 61 FPQPLPYQPSQPSQOQPEQVPLVQOQFPQOQOQFPQOQOQFPQOQOQFPQOQOQ 113
 QY 121 QOOLIPCMQVYLQOHNIHARSQVYLGSTYQLQELCCQHLMOIPESQCCAIHNVHAI 180
 DB 114 QOOLIPCMQVYLQOHNIHARSQVYLGSTYQLQELCCQHLMOIPESQCCAIHNVHAI 173
 QY 181 IHQOQKQOQSSQVSPQPLQOYPLGSGSPRSCQNPQAGSVQPLQOYPLQOY 240
 DB 174 IHQOQKQOQSSQVSPQPLQOYPLGSGSPRSCQNPQAGSVQPLQOYPLQOY 233
 QY 241 QTLFAMCNVYIAPYCTIAPFGIFGTN 266
 DB 234 QTLFAMCNVYIAPYCTIAPFGIFGTN 259

RESULT 14
 QY4M1 PRELIMINARY; PRT; 288 AA.
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Alpha-glialdin storage protein.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticaceae; Triticum.
 OC NCBI_Taxid=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cheyenne;
 RA Anderson O.D.;
 RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.

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GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: December 14, 2004, 17:00:05 ; Search time 76.6667 Seconds
(without alignments)
1244.635 Million cell updates/sec

Title: US-10-089-700-3-P65
Perfect score: 1433
Sequence: 1 VAVPVQLOPQNPSSQOQPE.....CNVYIAPYCTIAPFGIPTN 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseqp23Sep04:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1425	99.4	266	AAU01799	AAU01799 Wheat A-G
2	1425	99.4	266	ADH14513	ADH14513 A-glucan
3	1265.5	88.3	290	AAE38574	AAE38574 Wheat alp
4	1265.5	88.3	290	ADP19626	ADP19626 Alpha-2-G
5	463	32.3	369	AAW62647	AAW62647 Mature du
6	454.5	31.7	297	ADQ71669	ADQ71669 Amino aci
7	441.5	30.8	298	ADQ71661	ADQ71661 Amino aci
8	438.5	30.6	307	ADH89338	ADH89338 T. aestiv
9	438.5	30.6	307	ADG44134	ADG44134 T. aestiv
10	289.5	20.2	1798	ABH71695	ABH71695 Drosophi
11	271	18.9	2285	ABH63057	ABH63057 Drosophi
12	266	18.6	1162	AAV96255	AAV96255 Kaposi's
13	266	18.6	1162	AAV58500	AAV58500 HHV8 ORF
14	266	18.6	1162	AAH62331	AAH62331 Kaposi's
15	266	18.6	1162	ABH05621	ABH05621 Kaposi's
16	266	18.6	1162	ADJ65096	ADJ65096 HHV8 late
17	264.5	18.5	1069	ADQ30905	ADQ30905 Human pol
18	264.5	18.5	1069	ADQ30905	ADQ30905 Human pol
19	264.5	18.5	1069	ADQ30905	ADQ30905 Human pol
20	259	18.1	905	ABH53330	ABH53330 Protein s
21	259	18.1	905	ABH53330	ABH53330 Protein s
22	259	18.1	905	ADH89336	ADH89336 Disease t
23	253	17.7	186	ADH89336	ADH89336 H. vulgar
24	253	17.7	186	ADG44132	ADG44132 H. vulgar
25	253	17.7	260	ADQ47673	ADQ47673 Amino aci

ALIGNMENTS

26	248.5	17.3	900	4	ABH62018
27	242	16.9	1013	4	ABH71039
28	239	16.7	358	7	ABH65556
29	237.5	16.6	1069	4	ABH61305
30	237.5	16.6	1142	7	ADQ79968
31	236	16.5	2237	5	ABG70004
32	236	16.5	2703	4	ABH60074
33	231.5	16.2	149	4	AAH72673
34	231	16.1	160	7	ADH89335
35	231	16.1	160	8	ADG44131
36	231	16.1	4365	6	ABH38695
37	230.5	16.1	1902	6	ABH38695
38	230	16.1	1761	4	ABH59512
39	228	15.9	158	3	AAV54568
40	228	15.9	2280	4	ABH61650
41	228	15.9	4952	8	ADL25642
42	227	15.8	4952	5	ADH47759
43	227	15.8	4952	7	ADP68294
44	227	15.8	5159	5	ADH48828
45	226.5	15.8	863	4	ABH61004

RESULT 1
AAU01799 standard; protein, 266 AA.
ID AAU01799 standard; protein, 266 AA.

AAU01799;
07-SEP-2001 (first entry)

Wheat A-glucan.

Wheat; A-glucan; epitope; coeliac disease; gluten intolerance;
T-cell binding; antagonist; transglutaminase; transgenic plant.

Triticum aestivum.

WO200125793-A2.

12-APR-2001.

02-OCT-2000; 2000MO-GB003760.

01-OCT-1999; 99GB-00023306.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI, 2001-300179/31.

Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.

Claim 1; Page 52; 107pp; English.

The sequence represents wheat A-glucan. A-glucan derived peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and as antagonists to the peptides are useful for treating or preventing coeliac disease in an individual and for producing an antibody specific to them or a wild-type sequence. A mutant gliadin protein (or its fragment of 15 amino acids in length) whose wild-type sequence can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can

CC be modified by transglutaminase to a sequence that comprise the epitope
 CC is useful for decreasing the ability of gliadin protein to cause Coeliac
 CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
 CC binding of the epitopes are useful for obtaining a transgenic plant cell
 CC or seed and for the production of a protein. The resultant crop plant is
 CC useful for obtaining a product of a wheat plant, especially grain, which
 CC is optionally processed into flour or another grain product. Food
 CC comprising the antagonistic protein is useful instead of a wild-type
 CC gliadin

CC Sequence 266 AA;

Query Match 99.4%; Score 1425; DB 4; Length 266;

Best Local Similarity 99.6%; Pred. No. 2.5e-114; Mismatches 1; Indels 0; Gaps 0;

Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 VRYVPEQLQPNPSQQQPEQVPLVQQQFPQSQQQFPQCPYPQPPFPSPQPYLQLP 60
 1 VRYVPEQLQPNPSQQQPEQVPLVQQQFPQSQQQFPQCPYPQPPFPSPQPYLQLP 60
 DB 61 FQPPPLPYRPPQSPFPQCPYPQPPQYSPQPPISQQQAQQQQQQQQQQQQQQQQQQQQ 120
 61 FQPPPLPYRPPQSPFPQCPYPQPPQYSPQPPISQQQAQQQQQQQQQQQQQQQQQQQQ 120
 DB 121 QQLIPGMDVVLQOHNIAHARSQVLOQSTYQLQELCCOHLWQIPESQCOAHHNVVHAII 180
 121 QQLIPGMDVVLQOHNIAHARSQVLOQSTYQLQELCCOHLWQIPESQCOAHHNVVHAII 180
 DB 181 LHQOQKQKQKQSSQVSFQPPLOQYPLGQGSFRPSQONFQAQGSVPQQLPQFEERINLAL 240
 181 LHQOQKQKQKQSSQVSFQPPLOQYPLGQGSFRPSQONFQAQGSVPQQLPQFEERINLAL 240
 DB 241 QTLPMCMNYIAFYCTIAPFGIFGTN 266
 241 QTLPMCMNYIAFYCTIAPFGIFGTN 266

RESULT 2

ID ADH14513 standard; protein; 266 AA.

ADH14513;

11-MAR-2004 (first entry)

A-gliadin protein sequence SEQ ID NO:3.

coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

Synthetic.

WO2003104273-A2.

18-DEC-2003.

05-JUN-2003; 2003WC-GB002450.

05-JUN-2002; 2002GB-00012885.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2004-043640/04.

Preventing or treating coeliac disease comprises administering agent

which are wheat gliadin T cell epitope capable of being recognized by T

cell receptor.

Example 1; SEQ ID NO 3; 177bp; English.

The present invention describes a method (M1) for preventing or treating

CC coeliac disease. M1 comprises administering an agent (A) comprising a
 CC gliadin T cell epitope, which is capable of being recognised by a T cell
 CC receptor; to an individual. Gliadin is a component of gluten. (A) has
 CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
 CC be used in the preparation of a medicament for treating or preventing
 CC coeliac disease. (A) can also be used in the preparation of a diagnostic
 CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
 CC disease, in an individual, which involves determining whether T cells of
 CC the individual recognise the agent, recognition by the T cells indicating
 CC that the individual has, or is susceptible to, coeliac disease. The
 CC present sequence represents a protein which is used in the
 CC exemplification of the present invention.

CC Sequence 266 AA;

Query Match 99.4%; Score 1425; DB 8; Length 266;

Best Local Similarity 99.6%; Pred. No. 2.5e-114; Mismatches 1; Indels 0; Gaps 0;

Matches 265; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 1 VRYVPEQLQPNPSQQQPEQVPLVQQQFPQSQQQFPQCPYPQPPFPSPQPYLQLP 60
 1 VRYVPEQLQPNPSQQQPEQVPLVQQQFPQSQQQFPQCPYPQPPFPSPQPYLQLP 60
 DB 61 FQPPPLPYRPPQSPFPQCPYPQPPQYSPQPPISQQQAQQQQQQQQQQQQQQQQQQQQ 120
 61 FQPPPLPYRPPQSPFPQCPYPQPPQYSPQPPISQQQAQQQQQQQQQQQQQQQQQQQQ 120
 DB 121 QQLIPGMDVVLQOHNIAHARSQVLOQSTYQLQELCCOHLWQIPESQCOAHHNVVHAII 180
 121 QQLIPGMDVVLQOHNIAHARSQVLOQSTYQLQELCCOHLWQIPESQCOAHHNVVHAII 180
 DB 181 LHQOQKQKQKQSSQVSFQPPLOQYPLGQGSFRPSQONFQAQGSVPQQLPQFEERINLAL 240
 181 LHQOQKQKQKQSSQVSFQPPLOQYPLGQGSFRPSQONFQAQGSVPQQLPQFEERINLAL 240
 DB 241 QTLPMCMNYIAFYCTIAPFGIFGTN 266
 241 QTLPMCMNYIAFYCTIAPFGIFGTN 266

RESULT 3

ID AAE38574 standard; protein; 290 AA.

AAE38574;

04-DEC-2003 (first entry)

Wheat alpha-2 gliadin protein.

wheat; therapy; coeliac sprue; dermatitis herpetiformis; gluten toxicity;

glutenase; foodstuff; anti-inflammatory; dermatological; alpha-2 gliadin.

Trifolium aestivum.

WO2003068170-A2.

21-AUG-2003.

14-FEB-2003; 2003WC-US004743.

14-FEB-2002; 2002US-0357338P.

14-MAY-2002; 2002US-0380761P.

28-OCT-2002; 2002US-0392782P.

31-OCT-2002; 2002US-0422833P.

20-NOV-2002; 2002US-0428033P.

20-DEC-2002; 2002US-0435881P.

(STRD) UNIV IELAND STANFORD JUNIOR.

Hausch F, Gray G, Shan L, Khosla C;

WPI; 2003-697466/66.

XX Treating celiac sprue and/or dermatitis herpetiformis comprises
 PT administering to a patient a dose of a glutenase that attenuates gluten
 PT toxicity in the patient.
 XX
 PS Example 2; Fig 4; 69pp; English.
 XX
 CC The present invention relates to a method for treating celiac sprue
 CC and/or dermatitis herpetiformis. The method involves administering to a
 CC patient a dose of a glutenase that attenuates gluten toxicity in the
 CC patient. The method is also useful in treating a foodstuff to render the
 CC foodstuff less toxic to a celiac sprue patient. The present sequence is
 CC wheat alpha-2 gliadin protein used to illustrate the method of the
 CC invention
 CC
 XX
 SQ Sequence 290 AA;
 Query Match 88.3%; Score 1265.5; DB 7; Length 290;
 Best Local Similarity 84.7%; Pred. No. 1.4e-100;
 Matches 243; Conservative 8; Mismatches 15; Indels 21; Gaps 3;
 QY 1 VRVVPQLQPNPSQQQPEQVPLVQQQPFPGQQQFPFQQQPYQPQPFPSQQPYQLQP 60
 DB 2 VRVVPQLQPNPSQQQPEQVPLVQQQPFPGQQQFPFQQQPYQPQPFPSQQPYQLQP 61
 QY 61 F-----PPPLPYPQPSFPFQQPYQPQPFPSQQPYQPQPFPSQQPYQLQP 105
 DB 62 FPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQL 121
 QY 106 --QQQQQQQQQLLQQLLQQLLPCMDVYLQCHNIAHARSQVLAQSTYQLLELCCQHLMOI 163
 DB 122 QKQQQQQQQQQLLQQLLQQLLPCMDVYLQCHNIAHARSQVLAQSTYQLVQLCCQHLMOI 181
 QY 164 PEGSCCAIHNVVAHILH-----QQKQQQQPSSQVSFPQPLQOYVLGGGFRPSQQNPQ 219
 DB 182 PEGSRCAIHNVVAHILHQQQQQQQQQQQPLSQVSPQPLQOYVSGGSGFSPSQNPQ 241
 QY 220 AQSVPQQLPQFEIRNLALQTLPMCNVYIAPYCTIAPGIFGTN 266
 DB 242 AQSVPQQLPQFEIRNLALQTLPMCNVYIAPYCTIAPGIFGTN 288
 RESULT 4
 ADP19626
 ID ADP19626 standard; protein; 290 AA.
 XX
 AC ADP19626;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Alpha-2-gliadin protein, SEQ ID 28.
 XX
 KW Gluten; Celiac Sprue; wheat; gliadin; alpha-2-gliadin.
 XX
 OS Triticum aestivum.
 XX
 PN WO2004045392-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 20-NOV-2003; 2003WO-US037434.
 XX
 PR 20-NOV-2002; 2002US-0428033P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Khosla C, Shan L,
 XX
 DR WPI; 2004-460460/43.
 XX
 PT New gluten oligopeptides, useful for diagnosing Celiac Sprue, in
 PT diagnostic assays for detecting antibodies against such oligopeptides, or
 PT for producing antibodies that bind specifically to such oligopeptides.

XX Example 2; Fig 4; 50pp; English.
 XX
 CC The present invention relates to novel purified gluten oligopeptides. The
 CC gluten oligopeptides comprise multiple T cell or B cell epitopes
 CC (ADP19608, ADP19616-ADP19623). The gluten oligopeptides are useful in
 CC stimulating T cells from Celiac Sprue patients for diagnostic purposes,
 CC in diagnostic assays for detecting antibodies against such oligopeptides,
 CC or for producing antibodies that bind specifically to such oligopeptides.
 CC The present sequence was used to illustrate the invention.
 CC
 XX
 SQ Sequence 290 AA;
 Query Match 88.3%; Score 1265.5; DB 8; Length 290;
 Best Local Similarity 84.7%; Pred. No. 1.4e-100;
 Matches 243; Conservative 8; Mismatches 15; Indels 21; Gaps 3;
 QY 1 VRVVPQLQPNPSQQQPEQVPLVQQQPFPGQQQFPFQQQPYQPQPFPSQQPYQLQP 60
 DB 2 VRVVPQLQPNPSQQQPEQVPLVQQQPFPGQQQFPFQQQPYQPQPFPSQQPYQLQP 61
 QY 61 F-----PPPLPYPQPSFPFQQPYQPQPFPSQQPYQPQPFPSQQPYQLQP 105
 DB 62 FPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQLPYPQQL 121
 QY 106 --QQQQQQQQQLLQQLLQQLLPCMDVYLQCHNIAHARSQVLAQSTYQLLELCCQHLMOI 163
 DB 122 QKQQQQQQQQQLLQQLLQQLLPCMDVYLQCHNIAHARSQVLAQSTYQLVQLCCQHLMOI 181
 QY 164 PEGSCCAIHNVVAHILH-----QQKQQQQPSSQVSFPQPLQOYVLGGGFRPSQQNPQ 219
 DB 182 PEGSRCAIHNVVAHILHQQQQQQQQQQQPLSQVSPQPLQOYVSGGSGFSPSQNPQ 241
 QY 220 AQSVPQQLPQFEIRNLALQTLPMCNVYIAPYCTIAPGIFGTN 266
 DB 242 AQSVPQQLPQFEIRNLALQTLPMCNVYIAPYCTIAPGIFGTN 288
 RESULT 5
 AAW62647
 ID AAW62647 standard; protein; 369 AA.
 XX
 AC AAW62647;
 XX
 DT 17-OCT-2003 (revised)
 XX
 DT 25-MAR-2003 (revised)
 XX
 DT 09-OCT-1998 (first entry)
 XX
 DE Mature durum wheat glutenin protein.
 XX
 KW Glutenin gene; durum wheat; low-molecular-weight; transgenic durum wheat.
 XX
 OS Triticum turgidum subsp. durum.
 XX
 PN FR2757538-A1.
 XX
 PD 26-JUN-1998.
 XX
 PF 18-DEC-1997; 97FR-00016059.
 XX
 PR 19-DEC-1996; 96IT-MI002663.
 XX
 PA (ITUY-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
 XX
 PI D Ovidior, Forcedu E, Marchitelli C, Cardelli LE;
 XX
 DR WPI; 1998-365055/32.
 XX
 DR N-PSDB; AAV38816.
 XX
 PT Durum wheat glutenin gene - coding for glutenin protein of low molecular
 PT weight.
 PS Claim 8; Page 14; 18pp; French.

REF ID: A6281038

F1 DISULFIDE-BOND 22 /

CC No interference between the individual RNA sequences occur. This sequence
 CC represents a protein encoded by a target gene used in the method of the
 CC invention.

XX Sequence 307 AA;

Query Match 30.6%; Score 438.5; DB 7; Length 307;
 Best Local Similarity 42.8%; Pred. No. 1.9e-29;

Matches 125; Conservative 36; Mismatches 76; Indels 55; Gaps 16;

13 PSCQCPQEQVPLVQCCQFP-----GQQQQFPQCPYPCQPPSQQPYLQCPFPQPLP 67
 27 PGLERFWQCCPLPQCTFPQCPPLFSQCCQ-----QQLFPQCPFSQCCP-----PFVQCCGP 78
 66 YPQCPGFPQCP-----YPCPQYSPQCP-----SQQAQQCCQCCQCCQCCQCCQ 114
 79 PSCQCPPLPQCPFPSCQCCQVLPQ-----QPPSCQCCQVLPQCPFPQCCQCCQCCQ 137
 115 -LQQLIQQLIPCMQVVLQCH--NTAH-----ARSVLQOSTYQLIELCCQHLMOIPQS 167
 138 VQPSILQQLNFC-KVFLQCCSPVAMPQRLRSQMLQSSCHVMQCCQCCQCPQIPQS 196
 168 QCAIHNVVAHIIHQCCQCCQCCQSSQVSPQPLQCPYLGQSPFPSCQCP-----219
 197 RYEAIRATITVSTL--QEQCCVQGSIQSQCCQCPQ-----LGCCVSPQCCQCCQCCQ 251
 220 ---AQGS-VQPCQLPQFEIRNLALQTLPMQCVIAPY--CTIAPFGIFGT 265
 252 QQLAQGFPLQPHQIAQLEVMTSIALRILPTMCSVNVPLRTTTSVPFGV-GT 302

RESULT 9
 ADG44134
 ID ADG44134 standard; protein; 307 AA.

XX ADG44134;

DT 26-FEB-2004 (first entry);

XX T. aestivum glutenin-1D1 protein.

XX oil content; plant; storage protein; seed-specific promoter; 2S-albumin;
 XX 7S-globulin; 11S-globulin; 12S-globulin; zein-prolamine; transgenic;
 XX oil production; fat production; free fatty acid production; food;
 XX animal feed; pharmaceutical; fine chemical production; glutenin.

XX Triticum aestivum.

XX MO2003077643-A2.

XX 25-SEP-2003.

XX 17-MAR-2003; 2003WO-EP002733.

XX 20-MAR-2002; 2002DE-01012893.

XX (BAD1) BASF PLANT SCI GMBH.

XX Bauer U;

XX WPI; 2004-011465/01.

XX N-PSDB; ADG44133.

XX Increasing total oil content of plants, useful e.g. as foods or animal
 XX feeds, by reducing amount of storage proteins, particularly with double-
 XX stranded interfering RNA.

XX Claim 4; SEQ ID NO 174; 253pp; German.

XX This invention describes a novel method for increasing the total oil
 XX content of a plant by reducing the amount of at least one storage protein
 XX in the plant (or its tissue, organs, parts or cells) and selecting plants
 XX that have higher total oil content than starting plants. The storage

CC protein is suppressed by introducing antisense RNA, optionally combined
 CC with a ribozyme, sense RNA that induces co-suppression, DNA-binding
 CC factors directed against storage protein genes, viral sequences that
 CC degrade storage protein RNA, constructs that induce homologous
 CC recombination of endogenous storage protein genes or mutations into
 CC storage protein genes. Most preferably a plant cell is stably transfected
 CC with a recombinant expression construct, then regenerated to plants that
 CC express the incorporated sequence. The expression constructs particularly
 CC contain a seed-specific promoter and they are introduced into plants by
 CC standard methods, e.g. via Agrobacterium. The preferred storage proteins
 CC of the invention are 2S-albumins, 7S or 11S/12S-globulins or zein-
 CC prolamines. Transgenic organisms produced by the new method are used for
 CC production of oils, fats, free fatty acids or their derivatives, useful
 CC as foods, animal feeds, pharmaceuticals and fine chemicals. This sequence
 CC represents a storage protein used to illustrate the method of the
 CC invention.

XX Sequence 307 AA;

Query Match 30.6%; Score 438.5; DB 8; Length 307;
 Best Local Similarity 42.8%; Pred. No. 1.9e-29;

Matches 125; Conservative 36; Mismatches 76; Indels 55; Gaps 16;

13 PSCQCPQEQVPLVQCCQFP-----GQQQQFPQCPYPCQPPSQQPYLQCPFPQPLP 67
 27 PGLERFWQCCPLPQCTFPQCPPLFSQCCQ-----QQLFPQCPFSQCCP-----PFVQCCGP 78
 66 YPQCPGFPQCP-----YPCPQYSPQCP-----SQQAQQCCQCCQCCQCCQCCQ 114
 79 PSCQCPPLPQCPFPSCQCCQVLPQ-----QPPSCQCCQVLPQCPFPQCCQCCQCCQ 137
 115 -LQQLIQQLIPCMQVVLQCH--NTAH-----ARSVLQOSTYQLIELCCQHLMOIPQS 167
 138 VQPSILQQLNFC-KVFLQCCSPVAMPQRLRSQMLQSSCHVMQCCQCCQCPQIPQS 196
 168 QCAIHNVVAHIIHQCCQCCQCCQSSQVSPQPLQCPYLGQSPFPSCQCP-----219
 197 RYEAIRATITVSTL--QEQCCVQGSIQSQCCQCPQ-----LGCCVSPQCCQCCQCCQ 251
 220 ---AQGS-VQPCQLPQFEIRNLALQTLPMQCVIAPY--CTIAPFGIFGT 265
 252 QQLAQGFPLQPHQIAQLEVMTSIALRILPTMCSVNVPLRTTTSVPFGV-GT 302

RESULT 10

AB371695
 ID AB371695 standard; protein; 1798 AA.

XX AB371695;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polyprotein SFG ID NO 41877.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX MO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.
 XX 23-MAR-2000; 2000US-0191637P.
 XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter UC, Adams M, Li FMD, Myers EM;

XX WPI; 2001-656860/75.

DR N-PSDB; ABL15798.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 41877; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-
 CC ABL72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 1798 AA;
 Query Match 20.2%; Score 289.5; DB 4; Length 1798;
 Best Local Similarity 37.1%; Pred. No. 9e-16;
 Matches 99; Conservative 17; Mismatches 96; Indels 55; Gaps 11;
 QY 3 VPVPLQIQPNP-SQQPQEQVPLVQ-----CQQPFGQQQQPPPOQ 41
 Db 264 VPQCATPQQSFQSKFIDPTDVPVQVAVLSRSLSNODSLIMRQQLKQQQMQQQQQ 323
 QY 42 PYPQOPFP-SQQPYLQLQFPQ---PCLPYPQSPFPQPYPOPQYSPQSPISQQ 97
 Db 324 MAPPQQQQQAQQPQQQQQQQQPQQPQSPFPQQPPTTFLQQPQQNQMQ-IQQQ 382
 QY 98 QAQQQQQQQQQQQQQQILQQLP-CMDVVLQCH-NIAHRSQVLCQSTYQLIQ 153
 Db 383 QQQQQQQQQQQQQQQQVLTQQQPQPGQQQQVITQRHVINTSTAGCCQIISHSNL-- 440
 QY 154 ELCCGHLMOIPQSCCAHNVVAHILHQQKQKQQQSPSQVFPQPLQGYPLGQSPFR 213
 Db 441 -----ALQKQQQ-----LLHVQQQHQQQPQQQQQITVQQLPRAQQQQQLP 481
 QY 214 SQQNPAQSGVQPOLPQFEIRNLAL 240
 Db 482 QQHVVQQQ---QPPQV-QFTQQQQQIAL 504
 RESULT 11
 ABB63057
 ID ABB63057 standard; protein; 2285 AA.
 XX
 AC ABB63057;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 15963.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 XX
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;

XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL07160.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 15963; 21bp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-
 CC ABL72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 2285 AA;
 Query Match 18.9%; Score 271; DB 4; Length 2285;
 Best Local Similarity 35.7%; Pred. No. 4.6e-14;
 Matches 101; Conservative 14; Mismatches 104; Indels 64; Gaps 13;
 QY 7 QLPQPNP-----SQQPPQVPLVQQQQPFGQQQQPFPQPPYPOPQ---PFP-SQQP 54
 Db 909 QMQQQQPVAVAPTVNHQVMPQQQVN--QQQQQPPMQQQLPQQVQVQPPVLPFPQPHQPP 966
 QY 55 YLQ-QPFPQ-----PPLPYPQSPFPQPYPOPQYSPQSPISQQQA--- 99
 Db 967 QQQQQPQLQQQLQQLHMTVQAQBDL--TQQQMAQQQAQVYQQQQQCPQQAIVNNQQAIVAM 1024
 QY 100 QQQQQQQQQQQQQQQLLQQLI-----PCMDVVLQCHNIAHRSQVLCQSTYQLIQ 153
 Db 1025 QQAQGGQQQLSPLQIQQQILQQQVAVSHQQQIMQQQLAQHQQLQQQQQLQQQQQLQQQQ 1084
 QY 154 ELCCGHLMOIPQSCCAHNVVAHILHQQKQKQQQSPSQV---SPQPLQ-----QY 204
 Db 1085 QIQQQQLQQQQQLQQQ-QFYQQYQAQ--WPCQHQLVLGSGVMAPHQHQDQLQIPVQVQV 1141
 QY 205 PL-----GQSFPSPQNPQAQSGVQPOLPQF 232
 Db 1142 PPTSVAPPIQHTYVNOGGQVLTSDAQQQQHGFSAVPOQAAPF 1184
 RESULT 12
 AAY96255
 ID AAY96255 standard; protein; 1162 AA.
 XX
 AC AAY96255;
 XX
 DT 12-SEP-2003 (revised)
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Kaposi's sarcoma-associated herpesvirus LANA.
 XX
 KW Kaposi's sarcoma-associated herpesvirus; KSHV; rhadino virus;
 KW latency-associated nuclear antigen; LANA; gamma-2 herpes virus;
 KW human herpes virus 8; HHV8; rhadino virus cis-acting element; RVCAE;
 KW Kaposi's sarcoma; primary effusion lymphoma; PEL;
 KW human immunodeficiency virus; HIV; multicentric Castlemann's disease.
 XX
 OS Human herpesvirus 8.
 XX
 FH Key Location/Qualifiers
 FT Domain 14..17
 FT Domain /note="nuclear localisation signal, NLS"
 FT Domain 64..70
 FT Domain /note="nuclear localisation signal, NLS"
 FT Region 320..429

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Run on: December 14, 2004, 17:06:20 ; Search time 19 Seconds
(without alignments)
928.452 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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15: /cgn2_6/prodata/1/aa/5N_COMB.pep:*
16: /cgn2_6/prodata/1/aa/5O_COMB.pep:*
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21: /cgn2_6/prodata/1/aa/5T_COMB.pep:*
22: /cgn2_6/prodata/1/aa/5U_COMB.pep:*
23: /cgn2_6/prodata/1/aa/5V_COMB.pep:*
24: /cgn2_6/prodata/1/aa/5W_COMB.pep:*
25: /cgn2_6/prodata/1/aa/5X_COMB.pep:*
26: /cgn2_6/prodata/1/aa/5Y_COMB.pep:*
27: /cgn2_6/prodata/1/aa/5Z_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463	32.3	369	US-08-991-300-2	Sequence 2, Appl
2	266	18.6	1162	US-08-728-323A-2	Sequence 2, Appl
3	266	18.6	1162	US-09-298-568-2	Sequence 2, Appl
4	266	18.6	1162	US-09-410-399-2	Sequence 2, Appl
5	266	18.6	1162	US-09-894-273-2	Sequence 2, Appl
6	257	17.9	788	US-08-918-914-4	Sequence 4, Appl
7	234	16.3	256	US-08-248-796A-21251	Sequence 21251, A
8	231	16.1	498	US-09-270-767-45042	Sequence 45042, A
9	217	15.1	2074	US-09-491-356C-9	Sequence 9, Appl
10	216.5	15.1	579	US-09-668-119-3	Sequence 3, Appl
11	203.5	14.2	663	US-09-270-767-61220	Sequence 61220, A
12	203.5	14.2	1591	US-09-270-767-45698	Sequence 45698, A
13	202	14.1	2023	US-09-491-356C-8	Sequence 8, Appl
14	202	14.1	2124	US-09-538-092-1377	Sequence 1377, Ap
15	198.5	13.9	505	US-09-248-796A-19253	Sequence 19253, A
16	197.5	13.8	729	US-08-625-188-20	Sequence 20, Appl
17	197.5	13.8	2441	US-08-194-468-2	Sequence 2, Appl
18	197.5	13.8	2441	US-08-961-739-2	Sequence 2, Appl
19	197.5	13.8	2441	US-09-514-247A-8	Sequence 8, Appl
20	197.5	13.8	2441	US-09-686-316-2	Sequence 23759, A
21	196.5	13.7	379	US-09-248-796A-23759	Sequence 10, Appl
22	196.5	13.7	2442	US-09-514-247A-10	Sequence 1370, Ap
23	196.5	13.7	2442	US-09-248-796A-21017	Sequence 21017, A
24	196	13.7	216	US-09-248-796A-28087	Sequence 28087, A
25	187	13.0	316	US-09-270-767-42663	Sequence 42663, A
26	186.5	13.0	320	US-09-248-796A-24758	Sequence 24758, A
27	186.5	13.0	320	US-09-248-796A-24758	Sequence 24758, A

28	186	13.0	295	US-09-248-796A-20004	Sequence 20004, A
29	184.5	12.9	332	US-09-248-796A-21649	Sequence 21649, A
30	184	12.8	519	US-09-248-796A-19263	Sequence 19263, A
31	179.5	12.5	261	US-09-602-565-34	Sequence 34, Appl
32	178	12.4	383	US-09-248-796A-23236	Sequence 23236, A
33	178	12.4	408	US-09-248-796A-14480	Sequence 14480, A
34	178	12.4	1319	US-09-538-092-1291	Sequence 1291, Ap
35	177	12.4	848	US-09-538-092-33	Sequence 33, Appl
36	176.5	12.3	684	US-08-823-240A-9	Sequence 15319, A
37	176	12.3	618	US-09-248-796A-15319	Sequence 18720, A
38	175.5	12.2	382	US-09-248-796A-18720	Sequence 826, App
39	175	12.2	901	US-09-538-092-826	Sequence 19232, A
40	174	12.1	657	US-09-248-796A-19232	Sequence 37, Appl
41	173	12.1	1507	US-09-914-259-37	Sequence 2, Appl
42	171.5	12.0	903	US-08-853-310-2	Sequence 20699, A
43	171	11.9	675	US-09-248-796A-20699	Sequence 27827, A
44	169.5	11.8	311	US-09-248-796A-27827	Sequence 2, Appl
45	168.5	11.8	667	US-08-718-661-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-991-300-2
Sequence 2, Application US/08991300
Patent No. 5973225
GENERAL INFORMATION:
APPLICANT: D'OVUDIO, RENATO
APPLICANT: FORCEDU, ENRICO
APPLICANT: MERCHETTI, CINZIA
APPLICANT: CARDELLI, LUISA ERCOLI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF A GENE
TITLE OF INVENTION: ENCODING A LOW MOLECULAR WEIGHT GLUTENIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,300
FILING DATE: 16-DEC-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT MI 96/A 002663
FILING DATE: 19-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORVAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2264-0201-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-300-2
Query Match 32.3%, Score 463, DB 2, Length 369;
Best Local Similarity 40.2%, Pred. No. 1,7e-34;

Matches 134; Conservative 32; Mismatches 87; Indels 80; Gaps 14;

```
QY 6 PQLQPNPSSQGP---QGVPLVQGGPFGGQQGP---PQQYPPQPPF-----50
DB 38 PQQGCSQQQQPPLSQQQQPPFSQQQQPVLPPQPSFSQQQLPPFSQQQQPP 97
QY 51 ---SQGPYL-----QGFPPPLPYPPQGFPPQ-----PYQPQPPYSC 89
DB 98 PQQQQQVLPQPPSSQQQLPPFSQQQLPPFSQQQLPPFSQQQLPPFSQQ 157
QY 90 PQQPISQQQAQQQQQQQ-----QQQQQQQLQQ-----11QQQLIPCMAYLQ 132
DB 158 QQQPVLPPQPPFSQQQQQPIPPQPPFSQQQQPVLQQQIPFVHPSILQQQLNPC-KYFLQ 216
QY 133 QH-----NINARSOVLQGSTYGLJELCCGHLMOIPESQCOAHNVVHAIILHQOK 186
DB 217 QCCSWAMPQSLARSOQLQSSCHWQQQQCCQLPQLPQSGRYEIRIVSILL--QEQ 274
QY 187 QQQCPSQVFSQQLQYPLQGSFSPSQNPQAQS-----VQPPQLPFE 234
DB 275 QGVGSIQIQQQQPPQ---LGCVSQPPQQSQQLGQQPQQQLAHGTFLLQPHQIAQLV 331
QY 235 INNALQTLPMACNVYIAY--CTIAPFGIGT 265
DB 332 MTSIALRTLPMCMNVPLRYRTTTRVPPGV--GT 363
```

RESULT 2

US-08-728-323A-2

Sequence 2, Application US/08728323A

Patent No. 5948676

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Russek, Roy A.

APPLICANT: Moore, Patrick S.

APPLICANT: Edelman, Isidore S.

TITLE OF INVENTION: Immediate Early Protein From Kaposi's

TITLE OF INVENTION: Sarcoma-Associated Herpesvirus, DNA

TITLE OF INVENTION: Encoding Same And Uses Thereof

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/728,323A

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575/52268/JPW/NSC/SKS

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-278-0400

TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 1162 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-728-323A-2

Query Match

18.6%; Score 266; DB 2; Length 1162;

Best Local Similarity 38.0%; Pred. No. 6,4e-16;
Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

```
QY 4 PVLQLPQNPSSQGPQGVPLVQ---QGVPPGQ---QGVPPGQPPYPPQPPFSQQQLQ 59
DB 495 PQQGCSQQQQPPLSQQQQPPFSQQQQPVLPPQPSFSQQQLPPFSQQQQPP 553
QY 60 P---PQQP---PPLPYPPQ---PQSFPPQPPYPPQ---OPQVSOQPPISQQQAQQQQQQ 109
DB 554 PQQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQ 613
QY 110 QQQQQLLQQLLQQLLPCMVTVLQGNINARSOVLQGSTYGLJELCCGHLMOIPESQ 169
DB 614 EQQDEQQQDEQQ---QDEQQDEQQDEQQDEQQDEQQDEQQDE---QQDEQQQ 663
QY 170 QAHNVVHAIILHQOKQQQQPSQVFSQQLQYPLQGSFSPSQNPQAQSVPQQL 229
DB 664 EQQD-----EQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQ 716
QY 230 PPFEE 234
DB 717 EQQD 721
```

RESULT 3

US-09-298-568-2

Sequence 2, Application US/09298568

Patent No. 6322792

GENERAL INFORMATION:

APPLICANT: Kieff, Elliott D.

APPLICANT: Baltes, Mary E.

TITLE OF INVENTION: RHADINO VIRUS LANA ACTS IN TRANS ON A UNIT OF RHADINO

TITLE OF INVENTION: VIRUS DNA TO MEDIATE EFFICIENT EPISOME PERSISTENCE

FILE REFERENCE: 16412-10001R

CURRENT APPLICATION NUMBER: US/09/298,568

CURRENT FILING DATE: 1999-04-21

EARLIER APPLICATION NUMBER: US 60/109,422

EARLIER FILING DATE: 1998-11-19

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patent Ver. 2.0

SEQ ID NO 2

LENGTH: 1162

TYPE: PRT

ORGANISM: Kaposi's sarcoma-associated herpesvirus

US-09-298-568-2

Query Match 18.6%; Score 266; DB 3; Length 1162;
Best Local Similarity 38.0%; Pred. No. 6,4e-16;

Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10;

```
QY 4 PVLQLPQNPSSQGPQGVPLVQ---QGVPPGQ---QGVPPGQPPYPPQPPFSQQQLQ 59
DB 495 PQQGCSQQQQPPLSQQQQPPFSQQQQPVLPPQPSFSQQQLPPFSQQQQPP 553
QY 60 P---PQQP---PPLPYPPQ---PQSFPPQPPYPPQ---OPQVSOQPPISQQQAQQQQQQ 109
DB 554 PQQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQREPPQ 613
QY 110 QQQQQLLQQLLQQLLPCMVTVLQGNINARSOVLQGSTYGLJELCCGHLMOIPESQ 169
DB 614 EQQDEQQQDEQQ---QDEQQDEQQDEQQDEQQDEQQDEQQDE---QQDEQQQ 663
QY 170 QAHNVVHAIILHQOKQQQQPSQVFSQQLQYPLQGSFSPSQNPQAQSVPQQL 229
DB 664 EQQD-----EQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQDEQQQ 716
QY 230 PPFEE 234
DB 717 EQQD 721
```

RESULT 4


```

Query Match      18.6%; Score 266; DB 4; Length 1163;
Best Local Similarity 38.0%; Ptd. No. 6,4e-16;
Matches 93; Conservative 19; Mismatches 101; Indels 32; Gaps 10

QY 4 PYEQLOPQNSQQQPEQVPLVQ--QQQPFQQQ--QQPFQDPYPQPPPSQPIQLQ 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Query Match	17.9%;	Score 257;	DB 2;	Length 788;
Best Local Similarity	31.4%;	Pred. No. 2.6e-15;		
Matches	90;	Conservative	23;	Mismatches 96;
				Indels 78;
				Gaps 10

```

QY 2 RVPVPLQ-----PONSQQQPCQEYVAVQCCQFPFGQQQPPPCQPPPCQPPY 55
DB 201 RVPAPQAYARAEVYSAQ-----QQQPCQCCQRCQREHARLQCCQCCQ 252
QY 56 LQLPFPPLPPLPQPSFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 115
DB 253 QCCQCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 311
QY 116 QQTLLQQLPCMDVVLQCHNIAHARSQVLCQSTYLLQELCCQHLMOIPESQCCQALHN 175
DB 312 QCNFPQQ-----PQTTQFQSQQLQLQS-----GVVPQQH----- 342
QY 176 VHAIIHQCCQCCQPPSSQVS-----PQPLQCY-----PLQGSFR 212
DB 343 -----PQCCQPPQPPQLERSPDLQHAQYCCQMSQYENFQRAHAPAKADPCPGFCA 396
QY 213 PCCQNPQAGSVQPPQLPQFEIRNLALQTLPMQCNVYIAPCTIAP 259
DB 397 PVPQAPQQR-----RTPPPVLAVINATQ--PPLPQPPTRRPPAP 438

```

RESULT 7

US-09-248-796A-21251

Sequence 21251, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 21251

LENGTH: 256

TYPE: PRT

ORGANISM: Candida albicans

FEATURE:

NAME/KEY: UNSURE

LOCATION: (250)

OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno

US-09-248-796A-21251

Query Match

Best Local Similarity 36.8%; Score 234; DB 4; Length 256;

Matches 74; Conservative 11; Mismatches 66; Indels 50; Gaps 8;

```

QY 31 PCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 50
DB 75 PCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 119
QY 91 PCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 150
DB 120 PCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 160
QY 151 LQELCCQHLMOIPESQCCQALHNVAIILHQCCQCCQPPSSQVSFPQPLQCYVLAGS 210
DB 161 PCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 206
QY 211 FRPQQNPQAGSVQPPQLPQFEIRNLALQTLPMQCNVYIAPCTIAP 231
DB 207 QPPQQ--QLYKSPQPSFPQ 225

```

RESULT 8

US-09-270-767-45042

Sequence 45042, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

```

; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 45042
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-45042

```

Query Match 16.1%; Score 231; DB 4; Length 498;

Best Local Similarity 32.1%; Pred. No. 3,6e-13;

Matches 99; Conservative 20; Mismatches 101; Indels 88; Gaps 15;

```

QY 6 PQLQPNP-SQQPCQVPLVQCCQFPFGQQQPPPCQPPPCQPPY----- 57
DB 181 PQLQPNP-SQQPCQVPLVQCCQFPFGQQQPPPCQPPPCQPPY----- 235
QY 58 ---LQFPPLPPLPQPSFPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 105
DB 236 MQLRQPPQDPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 291
QY 106 QCCQCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 151
DB 292 QCCQCCQCCQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPP 348
QY 152 LQELCCQHLMOIPESQCCQALHNVAIILHQCCQCCQPPSSQVSFPQPLQCYVLAG 208
DB 349 LVETQHCHV-----QXQ-----HSGQVQVQPPQPPQLQDPSQGLPLY----- 386
QY 209 GSPFPQNPQA-----QSVQPPQLPQFEIRNLALQTLPMQCNVYIAPCTI 257
DB 387 HTMPPTSPVVTSPVLEQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 440
QY 258 APPGIFGT 265
DB 441 TPTGIAT 448

```

RESULT 9

US-09-491-356C-9

Sequence 9, Application US/09491356C

Patent No. 6566061

GENERAL INFORMATION:

APPLICANT: Philibert, Robert A.

APPLICANT: Gims, Edward I.

APPLICANT: Delist, Lynn

TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF X013

FILE REFERENCE: 9465, 6US11

CURRENT APPLICATION NUMBER: US/09/491,356C

CURRENT FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: PCT/US99/09365

PRIOR FILING DATE: 1999-04-29

PRIOR APPLICATION NUMBER: 6C/083,465

PRIOR FILING DATE: 1998-04-29

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.1

SEQ ID NO 9

LENGTH: 2074

TYPE: PRT

ORGANISM: Mus musculus

US-09-491-356C-9

Query Match

Best Local Similarity 15.1%; Score 217; DB 4; Length 2074;

Matches 87; Conservative 15; Mismatches 90; Indels 92; Gaps 10;

```

QY 7 QLPQNPNSQQQPPQVPLVQCCQFPFGQQQPPPCQPPPCQPPY-----PQPPFPSPQPPY 55

```


Db 1339 YGOP-----QISYKTLPMHPLAKSSLE-----SEIEKILANKGOSLAVV 1379

RESULT 13

US-09-491-356C-8
Sequence 8, Application US/09491356C
Patent No. 6566061

GENERAL INFORMATION:

APPLICANT: Philibert, Robert A.
APPLICANT: Gims, Edward I.

APPLICANT: Delisi, Lynn

TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13

FILE REFERENCE: 9465.6US11

CURRENT APPLICATION NUMBER: US/09/491,356C

CURRENT FILING DATE: 2000-01-26

PRIOR APPLICATION NUMBER: PCT/US99/09365

PRIOR FILING DATE: 1998-04-29

PRIOR APPLICATION NUMBER: 60/083,465

PRIOR FILING DATE: 1998-04-29

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.1

SEQ ID NO 8

LENGTH: 2023

TYPE: PRT

ORGANISM: Homo sapiens

US-09-491-356C-8

Query Match

Best Local Similarity 29.2%; Pred. No. 8, 6e-10;

Matches 87; Conservative 15; Mismatches 90; Indels 106; Gaps 11;

Db 1747 QQQPAVPGQGRLEQQ--LQSSGMLGSSVHOMTSSSGIGCTSGYTPYVSHVGLQHT 1804

44 ---PQPPFPSSQPPYLQPPFPPLPYP-----QPSPFPQPPYP----- 81

1805 GPAGTWPPSYSSQPPYQSTHPTNTPLVDFTNHLQRRSGVHQAAPYHGHLSTGRFS 1864

82 ---QPQPPYSG-----PQPSISQQAQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 117

1865 HQTLLQTPMISTMTSPMSAGVAGVASTALILEPQQQQQQQQQQQQQQQQQQQQQQ 1924

118 -ILQQQLIPCMVDVLIQGNHIAHARSQVLOQSTYQLLQELCCQHLWQIPESQCCAIHNVV 176

1925 HIRQQQ-----CCQILRQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 1962

177 HAILHQGXKQQ-----QPSGVVSFQ-QPLQGYPLGGSFRPSQGNPQAQGSVQPP 227

1963 ---HQQQQQQQAAPPPQPPQSPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 2015

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q93074
US-09-538-092-1377

Query Match

Best Local Similarity 14.1%; Score 202; DB 4; Length 2124;

Matches 87; Conservative 15; Mismatches 90; Indels 106; Gaps 11;

Db 7 QLOPQNPSSQPPQPPYLVQQQQFPQQQ--QQPFPQPPY----- 43

1847 QQQPAVPGQGRLEQQ--LQSSGMLGSSVHOMTSSSGIGCTSGYTPYVSHVGLQHT 1904

44 ---PQPPFPSSQPPYLQPPFPPLPYP-----QPSPFPQPPYP----- 81

1905 GPAGTWPPSYSSQPPYQSTHPTNTPLVDFTNHLQRRSGVHQAAPYHGHLSTGRFS 1964

82 ---QPQPPYSG-----PQPSISQQAQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 117

1965 HQTLLQTPMISTMTSPMSAGVAGVASTALILEPQQQQQQQQQQQQQQQQQQQQQQ 2024

118 -ILQQQLIPCMVDVLIQGNHIAHARSQVLOQSTYQLLQELCCQHLWQIPESQCCAIHNVV 176

2025 HIRQQQ-----CCQILRQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ 2062

177 HAILHQGXKQQ-----QPSGVVSFQ-QPLQGYPLGGSFRPSQGNPQAQGSVQPP 227

2063 ---HQQQQQQQAAPPPQPPQSPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 2115

Db

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Wed Dec 15 10:01:59 2004

Search completed: December 14, 2004, 17:29:04
Job time : 20 secs

us-10-089-700-3-p65.rat

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RESULT 5
US-10-474-955-101

Sequence 101, Application US/10474955
 Publication No. US20040241161A1
 GENERAL INFORMATION:
 APPLICANT: Drifhout, Jan W.
 APPLICANT: Konig, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS A
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 CURRENT FILING DATE: 2003-10-13
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 101
 LENGTH: 282
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of GAMMA-1
 US-10-474-955-101

Query Match
 Best Local Similarity 38.8%; Score 556.5; DB 17; Length 282;
 Matches 138; Conservative 32; Mismatches 73; Indels 47; Gaps 15;

QY 2 RVFVPL-----QPQNPQQPQEQVPLVQQQPFQ--Q--PPQPPPP--QPPS 51
 DB 10 QVFWQPP 68
 QY 52 --QQQYPL--LQPPPPPL--YPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 106
 DB 69 QPQYPP 118
 QY 107 QQQQQQQQLLQQLLPCMDVYLQGN---IAHRSQVLAQSTYQLLQELCCGHLWQ 162
 DB 119 FPOQPPSLIQSLQQLLPCMDVYLQGN---IAHRSQVLAQSTYQLLQELCCGHLWQ 178
 QY 163 IPESQCAHNVVAIIHQKQKQPPSSQVFPQPL--QYPLGGGSRFPQQNPQAQ 221
 DB 179 IPQQAIAHSHVSHIIMQEQEQEQ--GVQILPLVQQQVGGTL-----VQGG 229
 QY 222 GSVQPPQLPQFEIRNLALQTLPMCNVYIAPYCTI--APF-----GIFG 264
 DB 230 GICQPPAQLEAIRSLVLTPLTMCNVYVPPYECSTIRAPFSSVAGIGG 279

RESULT 6
 US-10-739-930-9621
 Sequence 9621, Application US/10739930
 Publication No. US20040216190A1
 GENERAL INFORMATION:
 APPLICANT: Kovalic, David K.
 TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
 FILE REFERENCE: 38-21(53377)B
 CURRENT APPLICATION NUMBER: US/10/739,930
 CURRENT FILING DATE: 2003-12-18
 NUMBER OF SEQ ID NOS: 11088
 SEQ ID NO 9621
 LENGTH: 296
 TYPE: PRT
 ORGANISM: Trifolium aestivum
 FEATURE:
 OTHER INFORMATION: Clone ID: TRIA-23APR03-C125_65.p
 US-10-739-930-9621

Query Match
 Best Local Similarity 38.1%; Score 545.5; DB 17; Length 298;
 Matches 134; Conservative 28; Mismatches 75; Indels 49; Gaps 14;

QY 4 PVPQLPQNPBQQPQEQVPLVQQQPFQ--Q--PPQPPPP--QPPS 61

DB 36 PVP--QHPPPSQP-----QTFPPQTFPHQPPQPFQPPQ--PQQPFLQPPQPF 84
 QY 62 P-QPPLPYPQPP 110
 DB 85 PQQPQQPYPQ-----QPQQPPFPQQLPQQPQQPQQPQQPQQPQQPQQPQQP 140
 QY 111 QQLLQQLLQQLLPCMDVYLQGN---IAHRSQVLAQSTYQLLQELCCGHLWQIPQ 166
 DB 141 QPPIQPSLQQQVPPCKNPLQCKPVSIVSSIMSWPQDQVWRQCCQQLAQIPQ 200
 QY 167 SQCAHNVVAIIHQKQKQPPSSQVFPQPL--QYPLGGGSRFPQQNPQAQSVQ 225
 DB 201 LQCAHHTVSHIIMQEQEQEQ--GVHILPLVQQQVGGTL-----VQGGIIT 251
 QY 226 PQQLPQFEIRNLALQTLPMCNVYIAPYCTI--APF-----GIFG 264
 DB 252 PQQPAQLEAIRSLVLTPLTMCNVYVPPYECSTIRAPFSSVAGIGG 279

RESULT 7
 US-10-474-955-97
 Sequence 97, Application US/10474955
 Publication No. US20040241161A1
 GENERAL INFORMATION:
 APPLICANT: Drifhout, Jan W.
 APPLICANT: Konig, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 CURRENT FILING DATE: 2003-10-13
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: Patent in version 3.1
 SEQ ID NO 97
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Consensus amino acid sequence
 US-10-474-955-97

Query Match
 Best Local Similarity 36.5%; Score 523; DB 17; Length 279;
 Matches 132; Conservative 26; Mismatches 76; Indels 52; Gaps 14;

QY 4 PVPQLPQNPBQQPQEQVPLVQQQPFQ--Q--PPQPPPP--QPPS 61
 DB 18 PVP--QHPPPSQP-----QTFPPQTFPHQPPQPFQPPQ--PQQPFLQPPQPF 66
 QY 62 P-QPPLPYPQPP 110
 DB 67 PQQPQQPYPQ-----QPQQPPFPQQLPQQPQQPQQPQQPQQPQQPQQPQQP 122
 QY 111 QQLLQQLLQQLLPCMDVYLQGN---IAHRSQVLAQSTYQLLQELCCGHLWQIPQ 166
 DB 123 QPPIQPSLQQQVPPCKNPLQCKPVSIVSSIMSWPQDQVWRQCCQQLAQIPQ 182
 QY 167 SQCAHNVVAIIHQKQKQPPSSQVFPQPL--QYPLGGGSRFPQQNPQAQSVQ 225
 DB 183 LQCAHHTVSHIIMQEQEQEQ--GVHILPLVQQQVGGTL-----VQGGIIT 230
 QY 226 PQQLPQFEIRNLALQTLPMCNVYIAPYCTI--APF-----GIFG 264
 DB 231 PQQPAQLEAIRSLVLTPLTMCNVYVPPYECSTIRAPFSSVAGIGG 276

RESULT 8
 US-10-474-955-99
 Sequence 99, Application US/10474955
 Publication No. US20040241161A1
 GENERAL INFORMATION:

APPLICANT: Drifhout, Jan W.
 APPLICANT: Koning, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 TITLE OF INVENTION: DO BINDING PROLAMINE-DERIVED PEPTIDES
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 CURRENT FILING DATE: 2003-10-13
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 99
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Amino acid sequence of GAMMA-4
 US-10-474-955-99

Query Match: 36.5%; Score 523; DB 17; Length 279;
 Best Local Similarity 46.2%; Pred. No. 1,1e-32;
 Matches 132; Conservative 26; Mismatches 76; Indels 52; Gaps 14;

4 PVPQLPQNPSSQCPQPEQVPLVQCCQFPSCQCCQFP--PQQPYPPQPPFPSSQCPYLQLPF 61
 18 PVP--QHPQPSQCP-----QTFPPQCPQTFHQPPQCPQPPQ--PQQPYLPQPPF 66
 62 PQQP-LPYPPQPSFPQPPQPPQ-----PQYSPQCPISQQAQ--QCCQCCQCCQ 110
 67 PQQPQPPQPPQ-----QPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 122
 111 QCCILQQLIQQQLIPCDVVLQGHN---IAHRSQVLAQSTYQLLQELCCGHLWQIPQ 166
 123 QPPFIPSLQQQVNPCKNPLQCKPVSIVSSLSMIMWQSDQVVRQSCQQLAQIPQ 182
 167 SQCAIHNVVAHIIHQQKQCCQPSQVSPQQL-QQYPLGGSFRRPSCQNPQAQSVQ 225
 183 LQCAIHVAHSHIIMQEQCC-----GWHILPLVQCCQVQGGTL-----VQGGIIG 230
 226 PQQLPQPEIRNLALQTLPAKCNVYIAPYCTI--APF-----GIRG 264
 231 PQQPAQLAIRSLVLTLPKCNVYVPECSIIKAFSSVAGIGG 276

RESULT 9

US-10-474-955-98
 Sequence 98, Application US/10474955
 Publication No. US20040241161A1

GENERAL INFORMATION:
 APPLICANT: Drifhout, Jan W.
 APPLICANT: Koning, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 TITLE OF INVENTION: DO BINDING PROLAMINE-DERIVED PEPTIDES
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 CURRENT FILING DATE: 2003-10-13
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 98
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Amino acid sequence of GAMMA-2
 US-10-474-955-98

Query Match: 36.2%; Score 519; DB 17; Length 279;
 Best Local Similarity 45.8%; Pred. No. 2.2e-32;
 Matches 131; Conservative 26; Mismatches 77; Indels 52; Gaps 14;

4 PVPQLPQNPSSQCPQPEQVPLVQCCQFPSCQCCQFP--PQQPYPPQPPFPSSQCPYLQLPF 61

18 PVP--QHPQPSQCP-----QTFPPQCPQTFHQPPQCPQPPQ--PQQPYLPQPPF 66
 62 P--QPPPYPPQPSFPQPPQPPQ-----PQYSPQCPISQQAQ--QCCQCCQCCQ 110
 67 PQQPQPPQPPQ-----QPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 122
 111 QCCILQQLIQQQLIPCDVVLQGHN---IAHRSQVLAQSTYQLLQELCCGHLWQIPQ 166
 123 QPPFIPSLQQQVNPCKNPLQCKPVSIVSSLSMIMWQSDQVVRQSCQQLAQIPQ 182
 167 SQCAIHNVVAHIIHQQKQCCQPSQVSPQQL-QQYPLGGSFRRPSCQNPQAQSVQ 225
 183 LQCAIHVAHSHIIMQEQCC-----GWHILPLVQCCQVQGGTL-----VQGGIIG 230
 226 PQQLPQPEIRNLALQTLPAKCNVYIAPYCTI--APF-----GIRG 264
 231 PQQPAQLAIRSLVLTLPKCNVYVPECSIIKAFSSVAGIGG 276

RESULT 10

US-10-474-955-100
 Sequence 100, Application US/10474955
 Publication No. US20040241161A1

GENERAL INFORMATION:
 APPLICANT: Drifhout, Jan W.
 APPLICANT: Koning, Frits
 APPLICANT: McAdam, Stephan N.
 APPLICANT: Ludwig, Solid Magne
 TITLE OF INVENTION: METHODS AND MEANS FOR USE OF HLA-DQ RESTRICTED T-CELL RECEPTORS
 TITLE OF INVENTION: DO BINDING PROLAMINE-DERIVED PEPTIDES
 FILE REFERENCE: 2799/71244-PCT-US
 CURRENT APPLICATION NUMBER: US/10/474,955
 CURRENT FILING DATE: 2003-10-13
 NUMBER OF SEQ ID NOS: 137
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 100
 LENGTH: 279
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Amino acid sequence of GAMMA-3
 US-10-474-955-100

Query Match: 36.2%; Score 519; DB 17; Length 279;
 Best Local Similarity 46.0%; Pred. No. 2.2e-32;
 Matches 131; Conservative 28; Mismatches 76; Indels 50; Gaps 14;

4 PVPQLPQNPSSQCPQPEQVPLVQCCQFPSCQCCQFP--PQQPYPPQPPFPSSQCPYLQLPF 61
 18 PVP--QHPQPSQCP-----QTFPPQCPQTFHQPPQCPQPPQ--PQQPYLPQPPF 66
 62 P--QPPPYPPQPSFPQPPQPPQ-----PQYSPQCPISQQAQ--QCCQCCQCCQ 110
 67 PQQPQPPQPPQ-----QPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQPPQ 123
 112 QCCILQQLIQQQLIPCDVVLQGHN---IAHRSQVLAQSTYQLLQELCCGHLWQIPQ 167
 124 PPFIPSLQQQVNPCKNPLQCKPVSIVSSLSMIMWQSDQVVRQSCQQLAQIPQ 183
 166 SQCAIHNVVAHIIHQQKQCCQPSQVSPQQL-QQYPLGGSFRRPSCQNPQAQSVQ 226
 184 QCAIHVAHSHIIMQEQCC-----GWHILPLVQCCQVQGGTL-----VQGGIIG 231
 227 QQLPQPEIRNLALQTLPAKCNVYIAPYCTI--APF-----GIRG 264
 232 QCPAQLAIRSLVLTLPKCNVYVPECSIIKAFSSVAGIGG 276

RESULT 11

US-10-739-930-9778
 Sequence 9778, Application US/10739930
 Publication No. US20040216190A1

[illegible][illegible]

```

RESULT 14
US-10-425-115-200100
/ Sequence 200100, Application US/10425115
/ Publication No. US20040214272A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
/ TITLE OF INVENTION: Plants
/ FILE REFERENCE: 38-41(5322)B
/ CURRENT APPLICATION NUMBER: US/10/425,115
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 369326
/

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311

C;Accession: S07924; C61218

D5 81 FQBPQFFPQLPYRQPEFISPRQFIYRQFEQEIFQEQEISQQQAQQQQQQQQQQQQ

D5 81 FQBPQFFPQLPYRQPEFISPRQFIYRQFEQEIFQEQEISQQQAQQQQQQQQQQQQ

QY 112 QGIIQQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 171
 DB 141 QGIIQQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 200
 QY 172 HNVVAHAIILHQGQKQSSQVSPQPLQGYPLGGSFRPSQGNPAQGSVQPLQ 231
 DB 201 HNVVAHAIILHQGQKQSSQVSPQPLQGYPLGGSFRPSQGNPAQGSVQPLQ 259
 QY 232 FEIRNLALQTLPMCNVYIAPYC--TIAFGIFGTN 266
 DB 260 FEIRNLALQTLPMCNVYIAPYC--TIAFGIFGTN 296

RESULT 9

A22364

alpha/beta-gliadin precursor (clone A42) - wheat

N.Alternate names: prolamin

C.Species: Triticum aestivum (common wheat)

C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C.Accession: A22364

R.Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A.Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA

A.Reference number: A92541; PMID:85234522; PMID:2989281

C.Accession: A22364

A.Molecule type: mRNA

A.Residues: 1-319 <OK>

A.Cross-references: UNIPROT:P04725; GB:M1073; NID:G170715; PID:AAA34278.1; PID:G170716

C.Superfamily: Gliadin

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-319/Product: alpha/beta-gliadin #status predicted <MAT>

Query Match 87.0%; Score 1246.5; DB 2; Length 319;

Best Local Similarity 81.9%; Pred. No. 1.6e-74;

Matches 245; Conservative 5; Mismatches 16; Indels 33; Gaps 4;

QY 1 VAVPVQLQPNPSQQLPQEQVPLVQQLQFPQCCQFPQCPYPQPFPSQGYLQLP 60
 DB 21 VAVPVQLQPNPSQQLPQEQVPLVQQLQFPQCCQFPQCPYPQPFPSQGYLQLP 80
 QY 61 PPO-----PPLPYPQPSFPQCPYPQPFPSQGYLQLP 114
 DB 81 PPOPPFPPLPYPQPSFPQCPYPQPFPSQGYLQLP 140
 QY 115 LQGIILQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 174
 DB 141 LQGIILQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 200
 QY 175 VVFAIILH-----QQQKQSSQVSPQPLQGYPLGGS 209
 DB 201 VVFAIILHQQQKQSSQVSPQPLQGYPLGGS 260
 QY 210 SFRPSQGNPAQGSVQPLQGYPLGGSFRPSQGNPAQGSVQPLQGYPLGGS 266
 DB 261 SFRPSQGNPAQGSVQPLQGYPLGGSFRPSQGNPAQGSVQPLQGYPLGGS 319

RESULT 10

G22364

alpha/beta-gliadin precursor (clone A212) - wheat

C.Species: Triticum aestivum (common wheat)

C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C.Accession: G22364

R.Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A.Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DNA

A.Reference number: A92541; PMID:85234522; PMID:2989281

C.Accession: G22364

A.Molecule type: mRNA

A.Residues: 1-319 <OK>

A.Cross-references: UNIPROT:P04722

C.Superfamily: Gliadin

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-319/Product: alpha/beta-gliadin #status predicted <MAT>
 Query Match 86.8%; Score 1243.5; DB 2; Length 319;
 Best Local Similarity 80.9%; Pred. No. 2.5e-74;
 Matches 242; Conservative 7; Mismatches 17; Indels 33; Gaps 4;

QY 1 VAVPVQLQPNPSQQLPQEQVPLVQQLQFPQCCQFPQCPYPQPFPSQGYLQLP 60
 DB 21 VAVPVQLQPNPSQQLPQEQVPLVQQLQFPQCCQFPQCPYPQPFPSQGYLQLP 80
 QY 61 PPO-----PPLPYPQPSFPQCPYPQPFPSQGYLQLP 114
 DB 81 PPOPPFPPLPYPQPSFPQCPYPQPFPSQGYLQLP 140
 QY 115 LQGIILQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 174
 DB 141 LQGIILQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 200
 QY 175 VVFAIILH-----QQQKQSSQVSPQPLQGYPLGGS 209
 DB 201 VVFAIILHQQQKQSSQVSPQPLQGYPLGGS 260
 QY 210 SFRPSQGNPAQGSVQPLQGYPLGGSFRPSQGNPAQGSVQPLQGYPLGGS 266
 DB 261 SFRPSQGNPAQGSVQPLQGYPLGGSFRPSQGNPAQGSVQPLQGYPLGGS 319

RESULT 11

T06500

alpha/beta-gliadin A-IV precursor - wheat

C.Species: Triticum aestivum (common wheat)

C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C.Accession: T06500

R.Okita, T.W.; Cheesbrough, V.; Reeves, C.D.

J. Biol. Chem. 260, 8203-8213, 1985

A.Title: Evolution and heterogeneity of the alpha/beta-type and gamma-type gliadin DN

A.Reference number: A92541; PMID:85234522; PMID:2989281

C.Accession: T06500

A.Molecule type: mRNA

A.Residues: 1-297 <OK>

A.Cross-references: UNIPROT:P04724; EMBL:M1075; NID:G170723; PID:AAA34282.1; PID:G170724

C.Superfamily: Gliadin

C.Keywords: seed; storage protein

F.1-20/Domain: signal sequence #status predicted <SIG>

F.21-297/Product: alpha/beta-gliadin A-IV #status predicted <MAT>

Query Match 86.1%; Score 1233.5; DB 2; Length 297;

Best Local Similarity 84.3%; Pred. No. 1e-73;

Matches 236; Conservative 9; Mismatches 18; Indels 17; Gaps 3;

QY 1 VAVPVQLQPNPSQQLPQEQVPLVQQLQFPQCCQFPQCPYPQPFPSQGYLQLP 60
 DB 21 VAVPVQLQPNPSQQLPQEQVPLVQQLQFPQCCQFPQCPYPQPFPSQGYLQLP 80
 QY 61 P-----PPLPYPQPSFPQCPYPQPFPSQGYLQLP 113
 DB 81 PPOPPFPPLPYPQPSFPQCPYPQPFPSQGYLQLP 137
 QY 114 LQGIILQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 173
 DB 138 LQGIILQQLIPGMDVVLQGHNTAHASQVLAQSTYQLQELCCGHLMOIPROSCQA 197
 QY 174 NVVVAHAIILH-----QQQKQSSQVSPQPLQGYPLGGSFRPSQGNPAQGSVQ 226
 DB 198 NVVVAHAIILHQQQKQSSQVSPQPLQGYPLGGSFRPSQGNPAQGSVQ 257
 QY 227 QQLPQFEIRNLALQTLPMCNVYIAPYC--TIAFGIFGTN 266
 DB 258 QQLPQFEIRNLALQTLPMCNVYIAPYC--TIAFGIFGTN 297

RESULT 12

Query Match	85.2%	Score 1221;	DB 2;	Length 326;
Best Local Similarity	77.8%;	Pred. No. 7 4e-73;		
Matches 238;	Conservative	9;	Mismatches 19;	Indels 40;
				Gaps 4

RESULT 13

Query Match	84.0%;	Score 1204;	DB 2;	Length 320;
Best Local Similarity	79.0%;	Pred. No. 9.3e-72;		
Matches 237; Conservative	11;	Mismatches 18;	Indels 34;	Gaps 5,

60 PFPQ-----PPLPYRQRFPSFPQRPYRQRPQYRSQRPQZPISQQQA-QQQQQQQQQQQQQQQ 113

RESULT 14

Query Match	83.4%;	Score 1181;	DB 2;	Length 282;
Best Local Similarity	84.8%;	Pred. No. 2.6e-70;		
Matches 228;	Conservative 11;	Mismatches 20;	Indels 10;	Gaps 4.

RESULT 15

A;Molecule type: mRNA

A,Residues: 1-292 <OKI>
A,Cross-references: UNIPROT:P04721

Superfamily: glialdin
R1-20/Domain: signal sequence #status predicted <SIG>
R1-21-292/Product: alpha/beta-glialdin #status predicted <MAT>

Query Match 80.5%; Score 1153.5; DB 2; Length 292;
Best Local Similarity 84.1%; Pred. No. 1.7e-68;
Matches 227; Conservative 2; Mismatches 10; Indels 31; Gaps 4;

```
QY 1 VAVPVFQLQPNPSQQQPEQVPLVQCCQFPGCCQFPFPQPYPOPPFPSSQPYLQLQP 60
    |||||
DB 21 VAVPVFQLQPNPSQQQPEQVPLVQCCQFPGCCQFPFPQPYPOPPFPSSQPYLQLQP 80
    |||||
QY 61 F--PQ---PELPYPQPSFPPQPYPCQPOXSOPOQPI--QQCAQQCCQCCQCCQCCQCCQ 114
    |||||
DB 81 FLPQPFPPQLPISQPFPPQPYPCQPOXSOPOQPI--QQCAQQCCQCCQCCQCCQCCQ 140
    |||||
QY 115 LQQLLQQLLPCMDVVLQGHNTAHARQVLAQSTYQLQLQLCCQHLWQIPESQCCQAIHN 174
    |||||
DB 141 LQQLLQQLLPCMDVVLQGHNTAHARQVLAQSTYQLQLQLCCQHLWQIPESQCCQAIHN 200
    |||||
QY 175 VVAATILH-----QQKQQQPSQVSCQPLQQYPLGGG 209
    |||||
DB 201 VVAATILHQQQQQQQEQKQQLQQQQQQQQLQQQQQKQQQPSQVSCQPLQQYPLGGG 260
    |||||
QY 210 SFRPSQNPQAQGSVPQQLPQFEIRNLA 239
    |||||
DB 261 SFRPSQNPQAQGSVPQQLPQFEIRNLA 290
    |||||
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Search completed: December 14, 2004, 17:27:02
Job time : 16 secs

141 000L1PCMDVVVLC0ANIYHGKSQVLCOSTYLLQSLCCQCHMDQIPEOSCCCAINNVHAI 200	DT 01-MAR-2004 (1)EMBLrel. 26, Last annotation update)
DE Alpha-g.i.iacdn.	

DT 01-MAR-2004 (TREMblrel. 26, last annotation update)
DE Alpha-gliadin.

Query Match	93.2%	Score 1335.5	DB 2	Length 289
Best Local Similarity	94.1%	Pred. No. 3.3e-72		
Matches 253	Conservative 1	Mismatches 12	Indels 3	Gaps 1
DR PRINTS; PRO0208; GLIADGLUTEN.				
DR PRINTS; PRO0209; GLIADIN.				
DR SMART; SM00499; AAI; 1.				
DR SEQUENCE 289 AA; 33349 MM; 5F577C9CD63874FA CRC64;				
QY 1 VRVVPVLOLOQONFSEQQQOECEVPLVQQQQQEFQGGQQQCFPPQCPYPQPOPFPSQCPYLQOP 60				
DB 21 VRVVPVLOLOQONFSEQQQOECEVPLVQQQQQEFQGGQQQCFPPQCPYPQPOPFPSQCPYLQOP 80				
QY 61 FPGPPLPYPOQSFPPPOQPPYPOPOYSOPQOPIS---QQQAQQQQQQQQQQQQQQQQQ 117				
DB 81 FPGPPLPYPOQSFPPPOQPPYPOPOYSOPQOPISQQQQQQQQQQQQQQQQQQQQQQQ 140				
QY 118 ILQQQLPCMDVNVLCQHNIHAASQVLCQSTYQLQRECCCHLMQIEFQSCCAIHWVH 177				
DB 141 ILQQQLPCMDVNVLCQHNIHGRQVLCQSTYQLQRECCCHLMQIEFQSCCAIHWVH 200				
QY 178 AIIHHQQCKQQQSSQVSEFQCPLOQYPLGGSFPSQONFQAQSVQPOQLPQFEETR 237				
DB 201 AIIHHQQCKQQQSSQVSEFQCPLOQYPLGGSFPSQONFQAQSVQPOQLPQFEETR 260				
QY 238 LALQTLPMQCNVYIAPYCTIAPFGIFGTN 266				
DB 261 LALQTLPMQCNVYIAPYCTIAPFGIFGTN 289				
RESULT 11				
Q9M4L9 PRELIMINARY; PRT; 270 AA.				
ID Q9M4L9				
AC Q9M4L9; 01-OCT-2000 (TREMBlrel. 15, Created)				
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DR 01-MAR-2004 (TREMBlrel. 26, Last annotation update)				
DE Alpha-glutadin.				
OS Triticum aestivum (wheat).				
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;				
OC Triticeae; Triticum.				
OX NCBI_Taxid=4565;				
RN [1]				
RP SEQUENCE FROM N.A.				
KC STRAIN=MJoelner; TISSUE=Endosperm;				
RA Arentz-Hansen E.H., McAdam S.N., Molberg O., Kristiansen C.,				
RA Solid L.M.;				
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.				
DR EMBL; AJ133609; CAB76961.1; -				
DR GO; GO:0045735; F:nutrient reservoir activity; IEA.				
DR InterPro; IPR003512; AAI.				
DR InterPro; IPR001576; Gliadin.				
DR InterPro; IPR001954; Gila_gluenin.				
DR Pfam; PF00234; TYP_alpha_amy1; 1.				
DR PRINTS; PRO0208; GLIADGLUTEN.				
DR PRINTS; PRO0209; GLIADIN.				
DR SMART; SM00499; AAI; 1.				
FT CHAIN 1 270 alpha-gliadin.				
FT SEQUENCE 270 AA; 31491 MM; 1DB4B55285FADF5 CRC64;				
Query Match	92.7%	Score 1328.5	DB 2	Length 270
Best Local Similarity	94.0%	Pred. No. 8.2e-72		
Matches 251	Conservative 3	Mismatches 12	Indels 1	Gaps 1
QY 1 VRVVPVLOLOQONFSEQQQOECEVPLVQQQQQEFQGGQQQCFPPQCPYPQPOPFPSQCPYLQOP 60				
DB 2 VRVVPVLOLOQONFSEQQQOECEVPLVQQQQQEFQGGQQQCFPPQCPYPQPOPFPSQCPYLQOP 61				
QY 61 FPGPPLPYPOQSFPPPOQPPYPOPOYSOPQOPISQQQAQQQQQQQQQQQQQQQQQ 119				
DB 62 FPGPPLPYPOQSFPPPOQPPYPOPOYSOPQOPISQQQAQQQQQQQQQQQQQQQQQ 121				

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 14, 2004, 17:00:05 / Search time 76.6667 Seconds
(without alignments)
1244.635 Million cell updates/sec

Title: US-10-089-700-3-R65

Sequence: 1 VRRVPPQLQPNPSQQQPOE.....CNVYIAPYCTIAPFGIFGTN 266

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1980s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1427	99.7	AAU01799	AAU01799 Wheat A-g
2	1427	99.7	ADH14513	ADH14513 A-gliadin
3	1267.5	88.6	AAH38574	AAH38574 Wheat alp
4	1267.5	88.6	ADP19626	ADP19626 Alpha-2-S
5	464	32.4	AAH62647	AAH62647 Mature du
6	450.5	31.5	AD071669	AD071669 Amino aci
7	440.5	30.8	ADH89338	ADH89338 T. aestiv
8	440.5	30.8	ADG44134	ADG44134 T. aestiv
9	437.5	30.6	AD071661	AD071661 Amino aci
10	288.5	20.2	ABH71695	ABH71695 Drosophi
11	273	19.1	AAH96255	AAH96255 Kaposi's
12	273	19.1	AAH58500	AAH58500 HIV8 ORF
13	273	19.1	AAH62331	AAH62331 Amino aci
14	273	19.1	AAH62331	AAH62331 Amino aci
15	273	19.1	AAH62331	AAH62331 Amino aci
16	270	18.9	ADH65096	ADH65096 HIV8 late
17	266.5	18.6	ABH63057	ABH63057 Drosophi
18	266.5	18.6	AD030905	AD030905 Human Pcl
19	266.5	18.6	AD007138	AD007138 Novel hum
20	266.5	18.6	ADJ37233	ADJ37233 Human nuc
21	258	18.0	AD047673	AD047673 Amino aci
22	255	17.8	ADH89336	ADH89336 H. vulgar
23	251	17.5	ADG44132	ADG44132 H. vulgar
24	251	17.5	ABG93053	ABG93053 S. cerevi
25	251	17.5	ABR53130	ABR53130 Protein s
			ADK62564	ADK62564 Disease t

26	249.5	17.4	900	4	ABH62018
27	242	16.9	1013	4	ABH71039
28	241	16.8	358	7	ADH65556
29	238.5	16.7	1069	4	ABH61305
30	237.5	16.6	1142	7	ADH07968
31	237	16.6	4365	6	ABU02252
32	233	16.3	160	7	ADH89335
33	233	16.3	160	8	ADG44131
34	233	16.3	2237	5	ABG70004
35	233	16.3	2703	4	ABH60074
36	231.5	16.2	149	4	ABH72673
37	231	16.1	1761	4	ABH59512
38	230	16.1	158	3	AAH54568
39	230	16.1	2280	4	ABH61650
40	227	15.9	738	5	ABG93140
41	226	15.8	153	3	AAH69495
42	226	15.8	1428	4	ABH70377
43	225.5	15.8	785	8	ADP98983
44	225	15.7	368	4	ABH63167
45	224	15.7	1237	3	AAH81609

ALIGNMENTS

RESULT 1

AAU01799 standard; protein, 266 AA.

AAU01799;

07-SEP-2001 (first entry)

Wheat A-gliadin.

Wheat; A-gliadin; epitope; coeliac disease; gluten intolerance; wheat; T-cell binding; antagonist; transglutaminase; transgenic plant.

Triticum aestivum.

WO20015793-A2.

12-APR-2001.

02-OCT-2000; 2000WO-GB003760.

01-OCT-1999; 99GB-00023306.

(ISIS-) ISIS INNOVATION LTD.

Anderson RP, Hill AVS, Jewell DP;

WPI; 2001-300179/31.

Diagnosing coeliac disease or susceptibility to the disease in an individual, by detecting in vitro or in vivo T cells which bind immunodominant T cell epitope obtained from naturally occurring homolog of gliadin.

Claim 1, Page 52; 107pp; English.

The sequence represents wheat A-gliadin. A-gliadin derived peptides of the invention are used to test mammalian (preferably human) susceptibility to coeliac disease (gluten intolerance). The peptides are contacted with a blood sample and T cell recognition measured, a positive T-cell recognition indicating a susceptibility to coeliac disease. The peptides are useful for inducing tolerance in an individual and as antigens to the peptides are useful for producing an antibody specific to the peptides in an individual and for producing an antibody preventing coeliac disease in an individual. A mutant gliadin protein (or its fragment of 15 or a wild-type sequence). A mutant gliadin protein can be modified by transglutaminase to a sequence that comprises the epitope, but which has been modified in such a way that it does not contain sequence which can

CC be modified by transglutaminase to a sequence that comprise the epitope
CC is useful for decreasing the ability of gliadin protein to cause Coeliac
CC disease. Nucleic acids encoding proteins antagonistic to the T-cell
CC binding of the epitopes are useful for obtaining a transgenic plant cell
CC or seed for the production of a protein. The resultant crop plant is
CC useful for obtaining a product of a wheat plant, especially grain, which
CC is optionally processed into flour or another grain product. Food
CC comprising the antagonistic protein is useful instead of a wild-type
CC gliadin

XX Sequence 266 AA;

SC Query Match

Best Local Similarity 99.7%; Score 1427; DB 4; Length 266;

Matches 265; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRVPVQLPQNPSSQSQQEQEVLVYQQQCFPQQQQQFPQQQPYPPQPFPSQCPYLQOP 60
DB 1 VRVPVQLPQNPSSQSQQEQEVLVYQQQCFPQQQQQFPQQQPYPPQPFPSQCPYLQOP 60
QY 61 FPQPRLPYPPQSPFPQCPYPPQCPYSPQPPISQQAQQAQQQQQQQQQQQQQLLQQLLQ 120
DB 61 FPQPRLPYPPQSPFPQCPYPPQCPYSPQPPISQQAQQAQQQQQQQQQQQLLQQLLQ 120
QY 121 QQLIPCMQDVYLQCHNIAHARSQVLTQOSTYQLLQELCCQHLWQIPBSQSCQAIHNVVAII 180
DB 121 QQLIPCMQDVYLQCHNIAHARSQVLTQOSTYQLLQELCCQHLWQIPBSQSCQAIHNVVAII 180
QY 181 LHQQQKQQQQSSQVSPFOQPLQOYPLGGSSFPSSQNPQAQGSVQPPQLPFEEIRNAL 240
DB 181 LHQQQKQQQQSSQVSPFOQPLQOYPLGGSSFPSSQNPQAQGSVQPPQLPFEEIRNAL 240
QY 241 QTLPAMCNVYIAPYCTIAPFGIFGTN 266
DB 241 QTLPAMCNVYIAPYCTIAPFGIFGTN 266

RESULT 2

ADH14513 ID ADH14513 standard; protein; 266 AA.

XX ADH14513;

XX 11-MAR-2004 (first entry)

XX A-gliadin protein sequence SEQ ID NO:3.

XX coeliac disease; gliadin; gliadin T cell epitope; gastrointestinal;

XX vaccine.

XX Synthetic.

XX WO2003104273-A2.

XX 18-DEC-2003.

XX 05-JUN-2003; 2003WO-GB002450.

XX 05-JUN-2002; 2002GB-00012885.

XX (ISIS-) ISIS INNOVATION LTD.

XX Anderson RP, Hill AVS, Jewell DP;

XX WPI; 2004-043640/04.

XX Preventing or treating coeliac disease comprises administering agent

XX which are wheat gliadin T cell epitope capable of being recognized by T

XX cell receptor.

XX Example 1; SEQ ID NO 3; 177pp; English.

XX The present invention describes a method (M1) for preventing or treating

CC coeliac disease. M1 comprises administering an agent (A) comprising a
CC gliadin T cell epitope, which is capable of being recognised by a T cell
CC receptor, to an individual. Gliadin is a component of gluten. The agent (A) has
CC gastrointestinal activity, and can be used in vaccines. The agent (A) can
CC be used in the preparation of a medicament for treating or preventing
CC coeliac disease. (A) can also be used in the preparation of a diagnostic
CC means for use in diagnosing coeliac disease, or susceptibility to coeliac
CC disease, in an individual, which involves determining whether T cells of
CC the individual recognise the agent, recognition by the T cells indicating
CC that the individual has, or is susceptible to, coeliac disease. The
CC present sequence represents a protein which is used in the
CC exemplification of the present invention.

XX Sequence 266 AA;

SC Query Match

Best Local Similarity 99.7%; Score 1427; DB 8; Length 266;

Matches 265; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VRVPVQLPQNPSSQSQQEQEVLVYQQQCFPQQQQQFPQQQPYPPQPFPSQCPYLQOP 60
DB 1 VRVPVQLPQNPSSQSQQEQEVLVYQQQCFPQQQQQFPQQQPYPPQPFPSQCPYLQOP 60
QY 61 FPQPRLPYPPQSPFPQCPYPPQCPYSPQPPISQQAQQAQQQQQQQQQQQLLQQLLQ 120
DB 61 FPQPRLPYPPQSPFPQCPYPPQCPYSPQPPISQQAQQAQQQQQQQQQQQLLQQLLQ 120
QY 121 QQLIPCMQDVYLQCHNIAHARSQVLTQOSTYQLLQELCCQHLWQIPBSQSCQAIHNVVAII 180
DB 121 QQLIPCMQDVYLQCHNIAHARSQVLTQOSTYQLLQELCCQHLWQIPBSQSCQAIHNVVAII 180
QY 181 LHQQQKQQQQSSQVSPFOQPLQOYPLGGSSFPSSQNPQAQGSVQPPQLPFEEIRNAL 240
DB 181 LHQQQKQQQQSSQVSPFOQPLQOYPLGGSSFPSSQNPQAQGSVQPPQLPFEEIRNAL 240
QY 241 QTLPAMCNVYIAPYCTIAPFGIFGTN 266
DB 241 QTLPAMCNVYIAPYCTIAPFGIFGTN 266

RESULT 3

AAE38574 ID AAE38574 standard; protein; 290 AA.

XX AAE38574;

XX 04-DEC-2003 (first entry)

XX Wheat alpha-2 gliadin protein.

XX wheat; therapy; celiac sprue; dermatitis herpetiformis; gluten toxicity;

XX glutenase; foodstuff; antiinflammatory; dermatological; alpha-2 gliadin.

XX Triticum aestivum.

XX WO2003068170-A2.

XX 21-AUG-2003.

XX 14-FEB-2003; 2003WO-US004743.

XX 14-FEB-2002; 2002US-0357239P.

XX 14-MAY-2002; 2002US-0380761P.

XX 28-JUN-2002; 2002US-0392782P.

XX 31-OCT-2002; 2002US-0422933P.

XX 20-NOV-2002; 2002US-0428033P.

XX 20-DEC-2002; 2002US-0435881P.

XX (STRD) UNIV ERLAND STANFORD JUNIOR.

XX Hausch F, Gray G, Shan L, Khosla C;

XX WPI; 2003-697466/66.

XX Treating celiac sprue and/or dermatitis herpetiformis comprises
 PT administering to a patient a dose of a glutenase that attenuates gluten
 PT toxicity in the patient.
 XX
 XX Example 2; Fig 4; 69pp; English.
 XX
 CC The present invention relates to a method for treating celiac sprue
 CC and/or dermatitis herpetiformis. The method involves administering to a
 CC patient a dose of a glutenase that attenuates gluten toxicity in the
 CC patient. The method is also useful in treating a foodstuff to render the
 CC foodstuff less toxic to a celiac sprue patient. The present sequence is
 CC wheat alpha-2 gliadin protein used to illustrate the method of the
 CC invention
 CC
 XX Sequence 290 AA;
 SQ
 Query Match 88.6%; Score 1267.5; DB 7; Length 290;
 Best Local Similarity 84.7%; Pred. No. 1.3e-100;
 Matches 243; Conservative 9; Mismatches 14; Indels 21; Gaps 3;
 QY 1 VRVVPQLQPNPQQQPOEQVPLVQQQPFPGQQQFPFQQQPYPPQPFPSQQPYLQLQP 60
 Db 2 VRVVPQLQPNPQQQPOEQVPLVQQQPFPGQQQFPFQQQPYPPQPFPSQQPYLQLQP 61
 QY 61 F-----PQRLPYPPQGSFPQQQPYPPQPYSPQPPISQQQAQQQQQQ- 105
 Db 62 FPQQLPYPPQQLPYPPQQLPYPPQPFPPQPPQPPQPPQPPISQQQAQQQQQQ 121
 QY 106 --QQQQQQQQQLLQQQLIPCDVYLQCHNIAHARSQVLCQSTYQLGLCCGHLMOI 163
 Db 122 QKQQQQQQQQQLLQQQLIPCDVYLQCHNIAHARSQVLCQSTYQLGLCCGHLMOI 181
 QY 164 PEGSQCAIHNVVAHILH----QQKQQQQPSSQVSFQQPLQQYPLGGGSRFPQQNPQ 219
 Db 182 PEGSRCAIHNVVAHILHQQQQQQQQQQQQQPLSQVSPQQQYPSGGGSRFPQQNPQ 241
 QY 220 AQSQVQPPQLPQFEIRNLALQTLPMQCNVYIAPYCTIAPFGIFGTN 266
 Db 242 AQSQVQPPQLPQFEIRNLALQTLPMQCNVYIAPYCTIAPVGIFGTN 288
 RESULT 4
 ADP19626
 ID ADP19626 standard; protein; 290 AA.
 XX
 AC ADP19626;
 XX
 DT 26-AUG-2004 (first entry)
 XX
 DE Alpha-2-gliadin protein, SEQ ID 28.
 XX
 KW Gluten; Celiac Sprue; wheat; gliadin; alpha-2-gliadin.
 XX
 OS Triticum aestivum.
 XX
 PN WO2004045392-A2.
 XX
 PD 03-JUN-2004.
 XX
 PF 20-NOV-2003; 2003WO-US037434.
 XX
 PR 20-NOV-2002; 2002US-0428033P.
 XX
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Knosla C, Shan L;
 XX
 DR WPI; 2004-460460/43.
 XX
 PT New gluten oligopeptides, useful for diagnosing Celiac Sprue, in
 PT diagnostic assays for detecting antibodies against such oligopeptides, or
 PT for producing antibodies that bind specifically to such oligopeptides.

XX
 PS Example 2; Fig 4; 50pp; English.
 XX
 CC The present invention relates to novel purified gluten oligopeptides. The
 CC gluten oligopeptides comprise multiple T cell or B cell epitopes
 CC (ADP19608, ADP19616-ADP19623). The gluten oligopeptides are useful in
 CC stimulating T cells from celiac sprue patients for diagnostic purposes,
 CC in diagnostic assays for detecting antibodies against such oligopeptides,
 CC or for producing antibodies that bind specifically to such oligopeptides.
 CC The present sequence was used to illustrate the invention.
 XX
 XX Sequence 290 AA;
 SQ
 Query Match 88.6%; Score 1267.5; DB 8; Length 290;
 Best Local Similarity 84.7%; Pred. No. 1.3e-100;
 Matches 243; Conservative 9; Mismatches 14; Indels 21; Gaps 3;
 QY 1 VRVVPQLQPNPQQQPOEQVPLVQQQPFPGQQQFPFQQQPYPPQPFPSQQPYLQLQP 60
 Db 2 VRVVPQLQPNPQQQPOEQVPLVQQQPFPGQQQFPFQQQPYPPQPFPSQQPYLQLQP 61
 QY 61 F-----PQRLPYPPQGSFPQQQPYPPQPYSPQPPISQQQAQQQQQQ- 105
 Db 62 FPQQLPYPPQQLPYPPQQLPYPPQPFPPQPPQPPQPPQPPISQQQAQQQQQQ 121
 QY 106 --QQQQQQQQQLLQQQLIPCDVYLQCHNIAHARSQVLCQSTYQLGLCCGHLMOI 163
 Db 122 QKQQQQQQQQQLLQQQLIPCDVYLQCHNIAHARSQVLCQSTYQLGLCCGHLMOI 181
 QY 164 PEGSQCAIHNVVAHILH----QQKQQQQPSSQVSFQQPLQQYPLGGGSRFPQQNPQ 219
 Db 182 PEGSRCAIHNVVAHILHQQQQQQQQQQQQQPLSQVSPQQQYPSGGGSRFPQQNPQ 241
 QY 220 AQSQVQPPQLPQFEIRNLALQTLPMQCNVYIAPYCTIAPFGIFGTN 266
 Db 242 AQSQVQPPQLPQFEIRNLALQTLPMQCNVYIAPYCTIAPVGIFGTN 288
 RESULT 5
 AAM62647
 ID AAM62647 standard; protein; 369 AA.
 XX
 AC AAM62647;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 09-OCT-1998 (first entry)
 XX
 DE Mature durum wheat glutenin protein.
 XX
 KW Glutenin gene; durum wheat; low-molecular-weight; transgenic durum wheat.
 XX
 OS Triticum turgidum subsp. durum.
 XX
 PN FR2757538-A1.
 XX
 PD 26-JUN-1998.
 XX
 PF 18-DEC-1997; 97FR-00016059.
 XX
 PR 19-DEC-1996; 96IT-MI002663.
 XX
 PA (ITUY-) ITAL MIN UNIV RICECA SCI & TECNOLOGICA.
 XX
 PI D Ovidior, Porceddu E, Marchitelli C, Cardelli LE,
 XX
 DR WPI; 1998-365055/32.
 DR N-PSDB; AAV38816.
 XX
 PT Durum wheat glutenin gene - coding for glutenin protein of low molecular
 PT weight.
 XX
 PS Claim 8; Page 14; 18pp; French.

The present sequence represents the mature glutenin protein. The DNA sequence encoding this protein is isolated from the genomic DNA of *Triticum durum* L. The gene codes for a low-molecular-weight glutenin protein and can be used to produce transgenic durum wheat plants with "better quality characteristics" (no details given). (Updated on 25-MAR-2003 to correct PI field.) (Updated on 17-OCT-2003 to standardise OS field)

Sequence 369 AA;

Query Match	Score	DB 2	Length
32.48;	464;	2;	369;

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Rest Local immutability 40.45%  Piped: No. 1, /e-53%
Matches 134; Conservative 32; Mismatches 871; Indels 80; Gaps 14

CY 6 POCAPGNPSQQGQ-----QECVPLVQVQQQCPFGQQQQCP--POCPYPPQPPFP----- 50
DB 38 PQQQPCGQQQQQQPPPLSQQQQQPPFSSQQQQQQPPFSSQQQQQPLVLPQGPFSQQQLPFFSQQQQP 97
CY 51 ----SQGFFYL-----QLAPPFPQRLPFPQGSFPQQ-----PYCPQPPQYSQ 89
DB 98 FSGQQQQQVLPQGSFSGQQQLPPFSSQQLPFPFSQQGQVLPQPQGPFSQQQPPFSSQQLPFFSQ 157
CY 90 PQGPISQQQAQQQQQQQQ-----QQQQQQQLQG-----LQQQLIPCMQVVLQ 132
DB 158 QQQPQVLPQGPFSQQQQQQCPPLPPQGPFPFSQQQQPVLLQQQIIPVHPSIIQQQLNPF-KVFLQ 216
CY 133 QH-----NIAHRSQVTLQOSTFYQLLQELCCCHMLQIPEQSSQCAIHHVVAIILHQQX 186
DB 217 QCGSPMAMPQSLARSGMLQQSSCHWQQQQCCQLPLQIPQGRYVAIRIVASITL--QEQ 274
CY 187 QQQQPPSSQVSFQQPFLQVPLQGGSFPFSQQQNFQAQGS-----VQPPQLPFFEB 234
DB 275 QQVQGS:QTFQQQQPQQ-----LGGCVSQPQQQSQQQLGQQPQQQQQLAHGTFPHQIAQLLEV 331
CY 235 IRNLALQTLPMQCNVVIAYP--CTIAPFGIECT 265
DB 332 MTSTIALKTLPTMCNANVPLIRITTRRVFSEV-CT 363

```

RESULT

AD071669 standard; protein; 297 AA.

AC
AD071669;

DT 12-AUG-2004 (first entry)

DE Amino acid sequence of a modified glutenin LMW subunit.

low molecular subunit; LMW subunit; glutenin;

KW gluten intolerance.

OS. *Triticum* sp.

10

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(MONS) MONSANTO AGRAR DEUT

PA (PURA-) PURATOS NV.

Hinzmann E, Wieser H, Stahl U;

WPI: 2004-402870/38.

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains.

[illegible]

DR N-PSDB; ADO71668.
XX
XX Novel nucleic acid comprising sequence encoding modified glutenin
PT polypeptide, useful for preparing modified glutenin polypeptide as
PT gliadin substitute in foodstuffs such as dough, pastries and waters.
XX
PS Claim 16; Fig 11; 43pp; English.

CC The present sequence represents a modified low molecular weight (LMW)
CC subunit of glutenin. The wild type subunit is designated clone LMW6, and
CC is isolated from wheat cultivar Cheyenne. The LMW polypeptide does not
CC contain the allergenic epitope QQQP, and shows some minor differences to
CC published sequences. It therefore represents a new allele for LMW subunit
CC genes. The LMW polypeptide was modified to produce modified glutenin
CC polypeptides of the invention. In these modified polypeptides one or more
CC cysteine residues responsible for intermolecular cross linking through
CC disulfide bridges are deleted or substituted. The modified glutenin
CC polypeptide is useful as a gliadin substitute. It is also useful in the
CC preparation of foodstuffs, such as flour or for the preparation of
CC pharmaceutical products, such as tablets, where the foodstuffs contain a
CC considerably reduced amount of gliadin proteins or no gliadin proteins.
CC Pharmaceutical compositions comprising the modified polypeptide of the
CC invention are useful for treating patients suffering from coeliac disease
CC or persons who are intolerant to gluten.

SQ Sequence 297 AA

Query Match	Score	DB	Length
31.5%	450.5	8	297

[illegible]

RESULT 7
ADH00330

ID	ADH89338	standard; protein; 307 AA
vv		

AC ADH89338;

DT 06-MAY-2004 (first entry)

DE T. aestivum LMW glutenin-1D1 protein

KW double-stranded RNA; storage protein; 2S-albumin; 7S-globulin;
KW 11S/12S-globulin; zein; prolamine; homogenisate metabolic pathway;
KW pharmaceutical; plant; abiotic stress; fatty acid composition;
KW lipid composition; oil composition; carbohydrate composition; colour
KW pigmentation; pathogen resistance; fruit ripening delay; aging;
KW male sterility; lignin; fibre; cotton; vitamin E synthesis;
KW caffeine; theophylline; theanine biosynthesis; glutenn.

PN WO2003078629-A1.